

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model.

Run on: March 14, 2003, 09:06:48 ; Search time 36 Seconds  
 (without alignments)  
 70.327 Million cell updates/sec

Searched: US-09-359-426C-2

Perfect score: 81 Sequence: 1 XEERTPLTTAAAXAPPVXNA 19

scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0 Total number of hits satisfying chosen parameters: 908470

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	76	93.8	19 AAW64480	P. aeruginosa prot
2	76	93.8	19 AAW64480	Pseudomonas aerugi
3	44	54.3	291 AAAG30091	Arabidopsis thal
4	44	54.3	292 AAAG30090	Arabidopsis thal
5	44	54.3	305 ABP52865	Escherichia coli p
6	44	54.3	306 AAB67588	Amino acid sequenc
7	44	54.3	427 AAC30089	Arabidopsis thal
8	42	51.9	172 AAC43604	Arabidopsis thal
9	42	51.9	215 AAC43603	Arabidopsis thal
10	51.9	332 AAC43602	Arabidopsis thal	AYV54314

## ALIGNMENTS

11	41	50.6	1012 22	ABB68926	Drosophila melanog
12	40	49.4	258 23	ABB48420	Listeria monocytog
13	40	49.4	445 22	AAU36108	Klebsiella pneumonia
14	40	49.4	498 15	AAR51691	HIV-type virus Mvp
15	40	49.4	498 20	AAW93076	HIV isolate 5180 g
16	40	49.4	788 22	ABB68933	Drosophila melanog
17	40	49.4	1473 22	ABB68924	Drosophila melanog
18	39.5	48.8	1793 22	ABB59613	Drosophila melanog
19	39.5	48.8	128 21	AAG39650	Arabidopsis thal
20	39	48.1	137 22	ABG23339	Novel human diagno
21	39	48.1	233 22	AAG91909	C glutamatic prote
22	39	48.1	321 23	AAE22281	Murine SPS-1 part
23	39	48.1	395 23	AAE22282	Murine tumour SPAS
24	39	48.1	395 23	AAE22283	Murine normal SPAS
25	38.5	47.5	842 22	ABB67966	Drosophila melanog
26	38	46.9	225 22	ABH71511	Drosophila melanog
27	38	46.9	229 22	ABN4775	Human protein sequ
28	38	46.9	229 23	ABR81876	Double strand RNA
29	38	46.9	229 23	AAU81227	Human lung cancer
30	38	46.9	261 22	ARG91455	C glutamic prote
31	38	46.9	277 22	AAU18229	Novel human DNA-bi
32	38	46.9	307 11	AAR07361	Phospholipase D to
33	38	46.9	521 15	ABR63672	Aldehyde-dehydroge
34	38	45.7	19 22	AAU27612	Human LEKTI prote
35	37	45.7	120 21	AAG18092	Arabidopsis thal
36	37	45.7	243 21	AAQ5456	Arabidopsis thal
37	37	45.7	326 22	AAW93916	Human polypeptide,
38	37	45.7	358 22	ABC01028	Novel human diagno
39	37	45.7	396 23	ABP28655	Streptococcus poly
40	37	45.7	440 22	ABG01280	Novel human diagno
41	37	45.7	456 21	AYV54289	Consensus sequence,
42	37	45.7	498 18	AW06454	Capsicum annuum ly
43	37	45.7	498 21	AYV54313	Amino acid sequenc
44	37	45.7	500 21	AYV54314	Amino acid sequenc
45	37	45.7	500 21	AYV54315	Amino acid sequenc



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**RESULT 4**

ID AAG30090 standard; Protein: 292 AA.

XX AAG30090; first entry

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 35911.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS ARA

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000FP-0301439.

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ID	AAB67588	standard; protein; 306 AA.	KW	termination sequence.
XX	AAB67588;		XX	Arabidopsis thaliana.
AC			OS	
XX			XX	
DT	29-MAY-2001	(first entry)	PN	EP1033405 - R2.
XX			XX	
DE	Amino acid sequence of a deoxyribokinase enzyme.		PD	06-SEP-2000.
XX			XX	
KW	Deoxyribonucleoside; deoxyribose 1-phosphate; thymidine phosphorylase; purine nucleoside phosphorylase; phosphopentose mutase; phosphopentose aldolase; deoxyribokinase; nucleoside 2-deoxyribosyltransferase.		PF	25-FEB-2000; 2000EP-0301439.
XX			PR	25-FEB-1999; 99US-0121825.
KW			PR	05-MAR-1999; 99US-0123188.
XX			PR	09-MAR-1999; 99US-0123548.
OS	Salmonella typhi.		PR	23-MAR-1999; 99US-0125788.
XX			PR	25-MAR-1999; 99US-0126264.
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PA	(HOF ) ROCHE DIAGNOSTICS GMBH.		PR	16-APR-1999; 99US-0130077.
PA	(INSP ) INST PASTER.		PR	19-APR-1999; 99US-0130449.
PA	(PHAR-) PHARMA-WALDHOFF GMBH & CO KG.		PR	21-APR-1999; 99US-0130510.
XX			PR	23-APR-1999; 99US-0130891.
PT	Tischer W, Ihlenfeldt H, Barzu O, Sakamoto H, Pistotnik E;		PR	23-APR-1999; 99US-0131449.
PI	Mariere P, Poche S;		PR	30-APR-1999; 99US-0132407.
XX			PR	04-MAY-1999; 99US-0132484.
WPI	2001-235026/24.		PR	05-MAY-1999; 99US-0132485.
DR	N-PSDB; AAF5544.		PR	06-MAY-1999; 99US-0132486.
XX	In vitro enzymatic synthesis of deoxyribonucleosides comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate -		PR	07-MAY-1999; 99US-0132487.
PT	PG	Disclosure; Page 59-61; 73pp; English.	PR	11-MAY-1999; 99US-0134218.
XX	The present sequence represents a deoxyribokinase enzyme. This enzyme is involved in the biosynthesis of deoxyribonucleosides, and is used in the method of the invention. The specification describes a method for the in vitro enzymatic synthesis of deoxyribonucleosides. The method comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate. Enzymes which may be used in the method of the invention include thymidine phosphorylase, purine nucleoside phosphorylase, phosphopentose mutase, phosphopentose aldolase, fructose 1,6-diphosphate aldolase, deoxyribokinase, and nucleoside 2-deoxyribosyltransferase.		PR	14-MAY-1999; 99US-0134219.
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### RESULT 8

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DT 18-Oct-2000 (first entry)  
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 54519.

KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS Arabidopsis thaliana.

EP1033405-A2.

PD 06-SEP-2000.

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XX AAG43602;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 54517.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 hybridisation assay; genetic mapping; gene expression control; promoter;  
 termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

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PR	12-JUL-1999;	99US-0142977.	PR	20-SEP-1999;	99US-0154039.
PR	13-JUL-1999;	99US-0143542.	PR	20-SEP-1999;	99US-0154039.
PR	14-JUL-1999;	99US-0143624.	PR	20-SEP-1999;	99US-0154039.
PR	15-JUL-1999;	99US-0144005.	PR	22-SEP-1999;	99US-0155139.
PR	16-JUL-1999;	99US-0144085.	PR	23-SEP-1999;	99US-0155486.
PR	16-JUL-1999;	99US-0144086.	PR	24-SEP-1999;	99US-0155659.
PR	19-JUL-1999;	99US-0144325.	PR	15-SEP-1999;	99US-0156458.
PR	19-JUL-1999;	99US-0144331.	PR	29-SEP-1999;	99US-0156596.
PR	19-JUL-1999;	99US-0144332.	PR	04-OCT-1999;	99US-0157117.
PR	19-JUL-1999;	99US-0144333.	PR	05-OCT-1999;	99US-015753.
PR	19-JUL-1999;	99US-0144334.	PR	06-OCT-1999;	99US-0157805.
PR	19-JUL-1999;	99US-0144335.	PR	07-OCT-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144335.	PR	08-OCT-1999;	99US-0158322.
PR	19-JUL-1999;	99US-0158669.	PR	12-OCT-1999;	99US-0158669.
PR	19-JUL-1999;	99US-0159393.	PR	13-OCT-1999;	99US-0159394.
PR	19-JUL-1999;	99US-0159395.	PR	13-OCT-1999;	99US-0159395.
PR	19-JUL-1999;	99US-0159396.	PR	14-OCT-1999;	99US-0159396.



CC and modulate L. monocytogenes-related diseases. In addition, the genome sequences and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.  
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

CC for homologous nucleic acids which are required for cell proliferation in  
CC a wide variety of organisms. The present sequence represents an  
CC prokaryotic cellular proliferation protein.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
format directly from WIPO at  
CC [ftp://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Query Match 49.4%; Score 40; DB 22; Length 445;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 EEKTPJLTAAAXPV 15  
 Db 382 EOKTPLAAADMAT 395

ID AUJ36108  
 AAU36108 standard; Protein; 445 AA.  
 XX  
 AC AAU36108;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Klebsiella pneumoniae cellular proliferation protein #96.  
 XX  
 KW antisense; prokaryotic cellular proliferation protein;  
 KW antibiotic resistance; cellular proliferation protein;

KUSOUL\_14  
 AAR51691  
 AAR51691 standard; Protein; 498 AA.  
 XX  
 AC  
 AAR51691;  
 XX  
 DT  
 07-NOV-1994 (first entry)  
 XX  
 DE  
 HIV-type virus MV5180/91 gag protein (cloned).  
 XX  
 KW  
 Human immunodeficiency virus; HIV; antigen; detection; diagnosis.

DE HIV-type virus MVP5180/91 gag protein (cloned).  
 XX KW Human immunodeficiency virus; HIV: antigen; detection; diagnosis;  
 KW retrovirus; vaccine; lymphocyte; reverse transcriptase.  
 XX OS HIV-type virus MVP-5180/91 (ECACC V92092318).  
 XX PN EP591914-A.  
 XX

21-MAR-2001; 2001WO-US09180.

PF  
VV  
05-OCT-1993; 93EP-0116058.

PR 23-MAY-2000; 2000US-206848P  
PR 26-MAY-2000; 2000US-207727P  
PR 23-OCT-2000; 2000US-242578P

PR 01-JUN-1993 93DE-4318186

ESTATE PLANNING

PI Brunn VA, Eberle J, Gurtler YY

I  
I  
I  
I  
X

Haselebeck R, Ohlisen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ; Yamamoto RT, Xu HH;

PT New HIV-type immune

New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.

MVR-5180/61

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in inhibiting prokaryotic cellular proliferation, and compositions containing such antisense inhibitors.

Western blots than the enzyme from HTLV-1 or CC virus. Although this is 3 to 7 kb smaller in transciptase (K<sub>m</sub>), it is about 10 times more active than the enzyme from HTLV-1.

genes themselves and the encoded proteins. The discovery of novel antibiotics, the essential

antibodies and its gp41 transmembrane protein, but more reactive than HIV-2, against p24-specific antibodies.

<sup>11</sup> Sera of African patients but not (or only weakly) with sera of German patients.

for antibiotic development. The antisense nucleic acid approach may also be useful for the identification of potential new targets

The virus consists of RNA in a peg-shaped core made of p24 subunits surrounded by an outer core of p17 subunits.

and *Escherichia coli* proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to these proteins.

which, apart from host-cell-derived lipids, comprises gp41 and envelope protein gp130 (which can bind to gp41).

antisense can be used to screen compounds in rational drug discovery programmes. The antisense molecule is a sequence of nucleic acids.

related viruses have at least 75% homology over the entire genome with max difference

us-09-359-426c-2.rag

CC 10%, POL 12%, GAG 14%, VIF 15% and ENV 22%.

Query	Match	Score	DB	Length
Best Local Similarity	49.4%	40	15	498
Matches	8	Pred.	No.	$1.5 \times 10^2$
Oy	EEKPLUTAXAPAVINX	19	Mismatches	7
Db	EETSPRQTSQVNPYIVNA	136	Indels	

RESULT  
AAW9307

ID AAW93076 standard; Protein; 498 AA.

HIV isolate 5180 gag protein.

**KW** HIV-type retrovirus; MNP-5180/91; ECACC V 92092310; antigen, assay  
**KW** detection; antibody; immune deficiency; vaccine.

Human immunodeficiency virus.

EP890642-A2.

PB  
XX  
13-JAN-1999.

xx  
PR 01-JUN-1993: 93DE-4318186.

PR 22-OCT-1992; 92DE-4235718.  
PR 22-OCT-1992; 93DE-1344541.

XX  
PA  
(DADE-) DADE BEHRING MARBURG GMBH.

PI Brunn AV, Eberle J, Guertler LG, Hauser H, Knapp S,  
XX

NEW HIV-TYPE RETROVIRUS

antigen used for detecting *Leishmania* spp. deficiency and to prepare vaccines.

Example 11; Fig 7; 39pp; German.

This invention describes the isolation of a novel HIV-type retrovirus called MVF-5180/91 (ECACC V 92092318). Antigens produced from this product can be used in an assay kit for detecting antibodies against viruses that cause immune deficiency, preferably where the assay is a Western blot, ELISA, or fluorescence immunoassay. MVF-5180/91, cDNA and/or antigen can be used for detecting retroviruses that cause immune deficiency and to prepare vaccines. This sequence represents an HIV MVF 5180 gag protein.

卷之三

Query	Match	Score	DB	Length
OY	2 EEKPLTIVAXAPVXNA	19	DB	20
	:   :   :   :			4000
Db	119 EETSPRQTSQNPYIVTNA	136		
Matches	8;	Conservative	3;	Mismatches
			7;	Indels
			0;	Gaps

search completed: March 14, 2003, 09:11:28  
Job time : 38 secs

Run on: OM protein - protein search, using sw model  
 March 14, 2003, 09:10:49 ; Search time 14 seconds  
 (without alignments)  
 39.931 Million cell updates/sec

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Title: US-09-359-426C-2  
 Perfect score: 81  
 Sequence: XBEKTPLTAAKAPVWNA 19  
 Scoring table: BLOSSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 26574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Listing first 45 summaries

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Length	DB ID
1	41	50.6	788 1 US-08-194-338-12
2	40	49.4	498 1 US-08-470-202-59
3	40	49.4	US-08-471-770-59
4	40	49.4	498 2 US-08-468-059-59
5	40	49.4	498 4 US-09-109-916-59
6	37	45.7	463 2 US-08-679-635A-4
7	37	45.7	463 4 US-09-419-163A-4
8	37	45.7	463 4 US-09-419-163A-4
9	36	44.4	493 3 US-08-943-173-8
10	36	44.4	58 3 US-08-943-173-16
11	36	44.4	71 3 US-08-943-173-2
12	36	44.4	181 4 US-09-117-237-19
13	36	44.4	181 4 US-08-945-476-19
14	36	44.4	181 4 US-09-489-352-19
15	36	44.4	182 4 US-09-117-237-48
16	36	44.4	182 4 US-09-489-352-48
17	35	44.4	236 4 US-09-134-001C 3558
18	36	44.4	355 2 US-08-458-555-2
19	36	44.4	610 1 US-07-821-717B-6
20	35	44.4	610 1 US-08-119-262B-6
21	36	44.4	610 1 US-08-135-529A-11
22	36	44.4	610 1 US-08-234-265A-11
23	35	44.4	2318 4 US-08-091-219-24
24	35	43.2	136 4 US-08-936-165A-61
25	35	43.2	223 4 US-09-009-816-4
26	35	43.2	225 4 US-09-071-035-204
27	35	43.2	4 US-08-818-112-142

RESULT 1  
 US-08-194-338-12  
 Sequence 12, Appl  
 Patent No. 5,474898  
 GENERAL INFORMATION:  
 APPLICANT: Venter, John C.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Fraser, Claire M.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: McCombie, William R.  
 TITLE OF INVENTION: OCTOPAMINE RECEPTOR  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson and Bear  
 STREET: 620 Newport Center Drive, Sixteenth Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/194,338  
 FILING DATE: 08-FEB-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/676,174  
 FILING DATE: 28-MAR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelson, Ned A.  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: NIH101.001DW1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 235-8550  
 TELEFAX: (619) 235-0176  
 INFORMATION FOR SEQ ID NO: 12:  
 SRQUENCE CHARACTERISTICS:  
 LENGTH: 788 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 Query Match Similarity 50.6%; Score 41; DB 1; Length 788;  
 Best Local Similarity 52.9%; Pred. No. 50; Length 788;

74

---

seconds  
its)  
self updates/sec

**ALIGNMENTS**

**RESULT<sup>1</sup>** US-08-194-338-12

; Sequence 12, Application US/08194338  
; Patent No. 5,474,898  
GENERAL INFORMATION:  
APPLICANT: Venter, John C.  
APPLICANT: Fraser, Claire M.  
APPLICANT: McCombie, William R.  
TITLE OF INVENTION: OCTOPAMINE RECEPTOR  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive, Sixteenth Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,338  
FILING DATE: 08-FEB-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,174  
FILING DATE: 28-MAR-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned A.

REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH101.001DW1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 788 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal

Query Match Similarity 50.6%; Score 41; DB 1; Length 788;  
Best Local Similarity 52.9%; Pred. No. 50;

US-08-194-338-12

RESULT 2  
 Sequence 59, Application US/08470202  
 Patent No. 5759808  
 GENERAL INFORMATION:  
 APPLICANT: Guertler, Lutz G.  
 APPLICANT: Eberle, Josef  
 APPLICANT: Brunn, Albrecht v.  
 APPLICANT: Knapp, Stefan  
 APPLICANT: Hauser, Hans-Peter  
 TITLE OF INVENTION: Retrovirus from the HIV Group and Its  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/470,202  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/132,653  
 FILING DATE: 05-OCT-1993  
 APPLICATION NUMBER: DE P 42 33 646.5  
 FILING DATE: 06-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 42 35 718.7  
 FILING DATE: 22-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 42 44 541.8  
 FILING DATE: 30-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 43 18 186.4  
 FILING DATE: 01-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michael J. Blake  
 REFERENCE/DOCKET NUMBER: 37,096  
 REFERENCE/DOCKET NUMBER: 05495-0001-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 498 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-470-202-59

Query Match 49.4%; Score 40; DB 1; Length 498;  
 Best Local Similarity 44.4%; Pred. No. 44; Indels 7; Gaps 0;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

RESULT 3  
 Sequence 59, Application US/08471770  
 Patent No. 5770427  
 GENERAL INFORMATION:  
 APPLICANT: Guertler, Lutz G.  
 APPLICANT: Eberle, Josef  
 APPLICANT: Brunn, Albrecht v.  
 APPLICANT: Knapp, Stefan  
 APPLICANT: Hauser, Hans-Peter  
 TITLE OF INVENTION: Retrovirus from the HIV Group and Its  
 NUMBER OF SEQUENCES: 63  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
 STREET: 1300 I Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,770  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/132,653  
 FILING DATE: 05-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 42 33 646.5  
 FILING DATE: 22-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 42 44 541.8  
 FILING DATE: 30-DEC-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 43 18 186.4  
 FILING DATE: 01-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carol P. Einaudi  
 REGISTRATION NUMBER: 32,220  
 REFERENCE/DOCKET NUMBER: 05495-0001-03000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 498 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-471-770-59

Query Match 49.4%; Score 40; DB 1; Length 498;  
 Best Local Similarity 44.4%; Pred. No. 44; Indels 7; Gaps 0;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 EKTPPLTTAAXAPVXNA 19  
 Db 119 EETSPROTQNYPVTNA 136

## RESULT 4

US-08-468-059-59

; Sequence 59, Application US/08468059

; Patent No. 5840480

## GENERAL INFORMATION:

; APPLICANT: Guertler, Lutz G.

; Eberle, Josef

; APPLICANT: Brunn, Albrecht v.

; APPLICANT: Hauser, Stefan

; TITLE OF INVENTION: Retrovirus from the HIV Group and Its

; TITLE OF INVENTION: Use

; NUMBER OF SEQUENCES: 63

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &amp;

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; FILING DATE: 05-OCT-1993

; CURRENT APPLICATION DATA:

; FILING DATE: US/08/468, 059

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; FILING DATE: 06-JUN-1995

; PRIORITY APPLICATION DATA:

; FILING DATE: 06-OCT-1992

; PRIORITY APPLICATION DATA:

; FILING DATE: 22-OCT-1992

; PRIORITY APPLICATION DATA:

; FILING DATE: 30-DEC-1992

; PRIORITY APPLICATION DATA:

; FILING DATE: 01-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Carol P. Elraudi

; REFERENCE/DOCKET NUMBER: 32, 220

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 498 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-468-059-59

## RESULT 6

US-09-109-916-59

; Sequence 59, Application US/09109916

; Patent No. 627561

## GENERAL INFORMATION:

; APPLICANT: Cunningham Jr., Francis X.

; APPLICANT: Sun, Zairen

; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND

; TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES

; NUMBER OF SEQUENCES: 21

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &amp; NEUSTADT,

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: Arlington

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

; FILING NUMBER: US/09/624, 125

; FILING DATE: 29-MAR-1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelder, Steven B.

; REFERENCE/DOCKET NUMBER: 30, 073

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 456 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-624-125-20

Query Match Score 37; DB 1; Length 456;  
 Best Local Similarity 72.7%; Pred. No. 1.3e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 8; Conservative

QY 9 TAAXAPVXNA 19  
 | | | | | | | |  
 Db 336 TLAAPVWNA 346

RESULT 7  
 Sequence 4, Application US/08679635A  
 Patent No. 5985643

GENERAL INFORMATION:  
 APPLICANT: Tomasz, Herminia

APPLICANT: Delencastre, Herminia  
 TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF  
 TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF  
 NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David A. Jackson, Esq.  
 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 CITY: Hackensack  
 STATE: New Jersey  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/419,163

FILING DATE: 10-JUL-1996  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-141

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/679,635A  
 FILING DATE: 10-JUL-1996  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-141

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 463 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-09-419-163-4

RESULT 9  
 Sequence 8, Application US/08943173-8  
 Patent No. 6048538

GENERAL INFORMATION:  
 APPLICANT: Wang, Chang Yi  
 APPLICANT: Shen, Fan  
 APPLICANT: Chen, Pei De

TITLE OF INVENTION: PEPTIDES DERIVED  
 TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF  
 TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS  
 TITLE OF INVENTION: DIAGNOSTIC REAGENTS  
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Maria C.H. Lin  
 STREET: 345 Park Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10154-0053

RESULT 8  
 Sequence 4, Application US/09419163  
 US-09-419-163-4

Query Match Score 37; DB 2; Length 463;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 8; Conservative

QY 8 TTAAAPLVQTA 19  
 | | | | | | | |  
 Db 382 TTAAAPLVQTA 393

RESULT 8  
 Sequence 4, Application US/09419163

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,173  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lin, Maria C.H.  
 REGISTRATION NUMBER: 29,323  
 REFERENCE/DOCKET NUMBER: 1151-4152  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEFAX: 212-751-6849  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-943-173-8

RESULT 10  
 US-08-943-173-16  
 ; Sequence 16, Application US/08/943173  
 ; Patent No. 6048538  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Chang Yi  
 APPLICANT: Shen, Fan  
 APPLICANT: Chen, Pei De  
 TITLE OF INVENTION: PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS  
 TITLE OF INVENTION: PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Maria C.H. Lin  
 STREET: 345 Park Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10154-0053

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,173  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lin, Maria C.H.  
 REGISTRATION NUMBER: 29,323  
 REFERENCE/DOCKET NUMBER: 1151-4152  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEFAX: 212-751-6849  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 71 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-943-173-2

Query Match  
 Best Local Similarity 44.4%; Score 36; DB 3; Length 58;  
 Matches 8; Conservative 53.3%; Pred. No. 18; 1; Mismatches 6; Indels 0; Gaps 0;  
 Qy 2 EEKPLTAAAXAPVV 16  
 Db 31 ERQPKLKVKAAPVV 45

RESULT 11  
 US-08-943-173-2  
 ; Sequence 2, Application US/08/943173  
 ; Patent No. 6048538  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Chang Yi  
 APPLICANT: Shen, Fan  
 APPLICANT: Chen, Pei De  
 TITLE OF INVENTION: PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS  
 TITLE OF INVENTION: PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Maria C.H. Lin  
 STREET: 345 Park Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10154-0053

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,173  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lin, Maria C.H.  
 REGISTRATION NUMBER: 29,323  
 REFERENCE/DOCKET NUMBER: 1151-4152  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEFAX: 212-751-6849  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 71 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-943-173-2

Query Match  
 Best Local Similarity 44.4%; Score 36; DB 3; Length 71;  
 Matches 8; Conservative 53.3%; Pred. No. 22; 1; Mismatches 6; Indels 0; Gaps 0;  
 Qy 2 EEKPLTAAAXAPVV 16  
 Db 31 ERQPKLKVKAAPVV 45

RESULT 12  
 US-09-117-257-19  
 ; Sequence 19, Application US/09/117257  
 ; Patent No. 6214355  
 ; GENERAL INFORMATION:  
 APPLICANT: Hock, Magnus  
 APPLICANT: Guo, Betty

ATTORNEY/AGENT INFORMATION:  
 NAME: Lin, Maria C.H.  
 REGISTRATION NUMBER: 29,323  
 REFERENCE/DOCKET NUMBER: 1151-4152  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-758-4800  
 TELEFAX: 212-751-6849  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 58 amino acids  
 TYPE: amino acid

APPLICANT: Hanson, Mark  
 TITLE OF INVENTION: Dbpa AND Dbpb COMPOSITIONS AND METHODS OF USE  
 FILE REFERENCE: 4210\_000500  
 CURRENT APPLICATION NUMBER: US/09/117,257  
 CURRENT FILING DATE: 1998-07-22  
 EARLIER APPLICATION NUMBER: PCT/US96/17081  
 EARLIER FILING DATE: 1996-10-22  
 EARLIER APPLICATION NUMBER: 08/589,711  
 EARLIER FILING DATE: 1996-01-22  
 EARLIER APPLICATION NUMBER: 08/427,023  
 EARLIER FILING DATE: 1995-04-24  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 19  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: *Borrelia afzelii*  
 US-09-117-257-19

Query Match Best Local Similarity | 44.4%; Score 36; DB 4; Length 181;  
 Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 Qy 3 EKTPPLTAAKAPVYXNA 19  
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 Db 139 EKTPPTTAEGITIKA 155

## RESULT 13

US-08-945-476-19

Sequence 19, Application US/08945476  
 Patent No. 6248517  
 GENERAL INFORMATION:  
 APPLICANT: DECORTIN BINDING PROTEIN COMPOSITIONS AND METHODS OF USE  
 TITLE OF INVENTION: COMPUTER READABLE FORM:  
 NUMBER OF SEQUENCES: 27  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/945,476  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/589,711  
 FILING DATE: 22-JAN-1996  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 181 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-945-476-19

## RESULT 14

US-09-489-352-19

Sequence 19, Application US/09489352  
 Patent No. 6312907  
 GENERAL INFORMATION:  
 APPLICANT: Hock, Magnus  
 APPLICANT: Guo, Betty  
 APPLICANT: Hanson, Mark  
 TITLE OF INVENTION: Dbpa AND Dbpb COMPOSITIONS AND METHODS OF USE  
 FILE REFERENCE: 4210\_000500  
 CURRENT APPLICATION NUMBER: US/09/489,352  
 CURRENT FILING DATE: 2000-01-21  
 EARLIER APPLICATION NUMBER: PCT/US96/17081  
 EARLIER FILING DATE: 1996-10-22  
 EARLIER APPLICATION NUMBER: 08/589,711  
 EARLIER FILING DATE: 1996-01-22  
 EARLIER APPLICATION NUMBER: 08/427,023  
 EARLIER FILING DATE: 1995-04-24  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 19  
 LENGTH: 181  
 TYPE: PRT  
 ORGANISM: *Borrelia afzelii*  
 US-09-489-352-19

## RESULT 15

US-09-117-257-48

Sequence 48, Application US/09117257  
 Patent No. 6214355  
 GENERAL INFORMATION:  
 APPLICANT: Hock, Magnus  
 APPLICANT: Guo, Betty  
 APPLICANT: Hanson, Mark  
 TITLE OF INVENTION: Dbpa AND Dbpb COMPOSITIONS AND METHODS OF USE  
 FILE REFERENCE: 4210\_000500  
 CURRENT APPLICATION NUMBER: US/09/117,257  
 CURRENT FILING DATE: 1998-07-22  
 EARLIER APPLICATION NUMBER: PCT/US96/17081  
 EARLIER FILING DATE: 1996-07-22  
 EARLIER APPLICATION NUMBER: 08/589,711  
 EARLIER FILING DATE: 1996-01-22  
 EARLIER APPLICATION NUMBER: 08/427,023  
 EARLIER FILING DATE: 1995-04-24  
 NUMBER OF SEQ ID NOS: 66  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 48  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: *Borrelia afzelii*  
 US-09-117-257-48

## RESULT 16

US-09-117-257-19

Query Match Best Local Similarity | 44.4%; Score 36; DB 4; Length 182;  
 Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
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 Db 139 EKTPPTTAEGITIKA 155

Search completed: March 14, 2003, 09:13:13  
 Job time: 15 secs

RESULT 14

US-09-489-352-19

Sequence 19, Application US/09489352

Patent No. 6312907

GENERAL INFORMATION:

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:12:34 ; Search time 13 Seconds

(without alignments)  
67,365 Million Cell updates/sec

Title: US-09-359-426C-2

Sequence score: 81

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Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:  
\* 1: /ccn2\_6/ptodata/2/pubbac/US08\_NE01\_PUB.pep:  
\* 2: /ccn2\_6/ptodata/2/pubbac/PCM\_NE01\_PUB.pep:  
\* 3: /ccn2\_6/ptodata/2/pubbac/US06\_NE01\_PUB.pep:  
\* 4: /ccn2\_6/ptodata/2/pubbac/US06\_PUBCOMB.pep:  
\* 5: /ccn2\_6/ptodata/2/pubbac/US07\_NE01\_PUB.pep:  
\* 6: /ccn2\_6/ptodata/2/pubbac/US07\_PUBCOMB.pep:  
\* 7: /ccn2\_6/ptodata/2/pubbac/PCMUS\_PUBCOMB.pep:  
\* 8: /ccn2\_6/ptodata/2/pubbac/US08\_PUBCOMB.pep:  
\* 9: /ccn2\_6/ptodata/2/pubbac/US09\_NE01\_PUB.pep:  
\* 10: /ccn2\_6/ptodata/2/pubbac/US09\_PUBCOMB.pep:  
\* 11: /ccn2\_6/ptodata/2/pubbac/US10\_NE01\_PUBCOMB.pep:  
\* 12: /ccn2\_6/ptodata/2/pubbac/US10\_PUBCOMB.pep:  
\* 13: /ccn2\_6/ptodata/2/pubbac/US60\_NE01\_PUB.pep:  
\* 14: /ccn2\_6/ptodata/2/pubbac/US60\_PUBCOMB.pep:  
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Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	41	50.6	132	12	US-10-078-929-22
2	41	50.6	132	12	Sequence 22, Appl
3	40	49.4	132	12	Sequence 198, App
4	40	49.4	145	10	Sequence 11701, A
5	40	49.4	498	9	Sequence 59, Appl
6	40	49.4	498	9	Sequence 59, Appl
7	40	49.4	498	9	Sequence 59, Appl
8	39	48.1	155	10	Sequence 59, Appl
9	39	48.1	155	10	Sequence 2, Appl
10	39	48.1	233	9	Sequence 16, Appl
11	39	48.1	395	10	Sequence 5663, Appl
12	39	48.1	395	10	Sequence 19, Appl
13	38	46.9	229	10	Sequence 21, Appl
14	38	46.9	261	9	Sequence 92, Appl
15	38	46.9	10	US-09-952-432A-2	Sequence 5, Appl
16	37	45.7	277	10	Sequence 214, Appl
17	37	45.7	456	10	Sequence 20, Appl
18	37	45.7	498	10	Sequence 57, Appl
19	37	45.7	500	10	Sequence 58, Appl
20	37	45.7	500	10	Sequence 59, Appl

### ALIGNMENTS

RESULT 1	US-10-078-929-22	Sequence 55, Appl
	; Sequence 22, Application US/10078929	Sequence 964, Appl
	; Patent No. US20020152497A1	Sequence 2235, A
	; GENERAL INFORMATION:	Sequence 461, Appl
	; APPLICANT: Rafalski, Antoni	Sequence 3648, Ap
	; APPLICANT: Miao, Guo-Hua	Sequence 222, Appl
	; APPLICANT: Falco, Saverio Carl	Sequence 2, Appl
	; APPLICANT: Sakai, Harime	Sequence 224, App
	; APPLICANT: Ramdu, Ohmelayo O.	Sequence 6239, Ap
	; APPLICANT: Odeil, Joan T.	Sequence 224, Appl
	; APPLICANT: Meyer, Blake	Sequence 31, Appl
	; APPLICANT: Thorpe, Catherine	Sequence 6, Appl
	; APPLICANT: Weng, Zude	Sequence 44350, A
	; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in Stress Response	Sequence 136, App
	; FILE REFERENCE: BB1357 US NA	Sequence 17, Appl

CURRENT APPLICATION NUMBER: US10/078, 929	PRIOR APPLICATION NUMBER: 09/566, 394	PRIOR FILING DATE: 2000-02-19
PRIOR FILING DATE: 2000-03-05	PRIOR APPLICATION NUMBER: 60/133038	PRIOR APPLICATION NUMBER: 1999-05-07
PRIOR FILING DATE: 1999-05-07	PRIOR APPLICATION NUMBER: 60/133042	PRIOR FILING DATE: 1999-05-07
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PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133525	PRIOR APPLICATION NUMBER: 60/133525
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133526	PRIOR APPLICATION NUMBER: 60/133526
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133527	PRIOR APPLICATION NUMBER: 60/133527
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133528	PRIOR APPLICATION NUMBER: 60/133528
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133529	PRIOR APPLICATION NUMBER: 60/133529
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133530	PRIOR APPLICATION NUMBER: 60/133530
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133531	PRIOR APPLICATION NUMBER: 60/133531
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133532	PRIOR APPLICATION NUMBER: 60/133532
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133533	PRIOR APPLICATION NUMBER: 60/133533
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133534	PRIOR APPLICATION NUMBER: 60/133534
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133535	PRIOR APPLICATION NUMBER: 60/133535
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133536	PRIOR APPLICATION NUMBER: 60/133536
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133537	PRIOR APPLICATION NUMBER: 60/133537
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133538	PRIOR APPLICATION NUMBER: 60/133538
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133539	PRIOR APPLICATION NUMBER: 60/133539
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133540	PRIOR APPLICATION NUMBER: 60/133540
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133541	PRIOR APPLICATION NUMBER: 60/133541
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/133542	PRIOR APPLICATION NUMBER: 60/133542
PRIOR FILING DATE: 1999-05-11	PRIOR APPLICATION NUMBER: 60/1335	

RESULT 2  
US-10-078-929-198  
; Sequence 198, Application US/10078929  
; Patent No. US2002015297A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, John T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; FILE REFERENCE: BB1357 US NA  
; CURRENT APPLICATION NUMBER: US/10/078,929  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO: 198  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; US-10-078-929-198

RESULT 3  
US-09-815-242-11701  
; Sequence 198, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselebeck, Robert  
; APPLICANT: Ohlsen, Kari L.

RESULT 4  
US-09-886-156-59  
; Sequence 59, Application US/09886156  
; Patent No. US20020155428A1  
; GENERAL INFORMATION:  
; APPLICANT: Guertler, Lutz G.  
; APPLICANT: Eberle, Josef  
; APPLICANT: Brunn, Albrecht V.  
; APPLICANT: Knapp, Stefan  
; APPLICANT: Hauser, Hans-Peter  
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
; FILE REFERENCE: 03495.001-04  
; CURRENT APPLICATION NUMBER: US/09/886,156  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US/09/1109,916  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
; PRIOR FILING DATE: 1992-10-06  
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7  
; PRIOR FILING DATE: 1992-10-22  
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
; PRIOR FILING DATE: 1992-12-30  
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
; PRIOR FILING DATE: 1993-06-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 59  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
; US-09-886-156-59

Query Match 49.4%; Score 40; DB 9; Length 498;  
 Best Local Similarity 44.4%; Pred. No. 25;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 EEKPLTTAAAXAPVXNA 19  
 Db 119 EETSPROTSONYPIVTNA 136

---

RESULT 5  
 US-09-886-150-59  
 Sequence 59, Application US/09886150  
 PATENT NO. US20020172939A1  
 GENERAL INFORMATION:  
 APPLICANT: Guertler, Lutz G.  
 APPLICANT: Ebner, Josef  
 APPLICANT: Brunn, Albrecht V.  
 APPLICANT: Knapp, Stefan  
 APPLICANT: Hauser, Hans-Peter  
 TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
 FILE REFERENCE: 05495\_0001-04  
 CURRENT APPLICATION NUMBER: US/09/886,150  
 CURRENT FILING DATE: 2001-06-22  
 PRIOR APPLICATION NUMBER: 05/109,916  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
 PRIOR FILING DATE: 1992-10-06  
 PRIOR APPLICATION NUMBER: DE P 42 35 718.7  
 PRIOR FILING DATE: 1992-10-22  
 PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
 PRIOR FILING DATE: 1992-12-30  
 PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
 PRIOR FILING DATE: 1993-06-01  
 NUMBER OF SEQ ID NOS: 67  
 SOFTWARE: Patentin ver. 2.0  
 SEQ ID NO 59  
 LENGTH: 498  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus  
 US-09-886-150-59

Query Match 49.4%; Score 40; DB 9; Length 498;  
 Best Local Similarity 44.4%; Pred. No. 25;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 EEKPLTTAAAXAPVXNA 19  
 Db 119 EETSPROTSONYPIVTNA 136

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RESULT 6  
 US-09-886-149-59  
 Sequence 59, Application US/09886149  
 PATENT NO. US200300342A1  
 GENERAL INFORMATION:  
 APPLICANT: Guertler, Lutz G.  
 APPLICANT: Ebner, Josef  
 APPLICANT: Brunn, Albrecht V.  
 APPLICANT: Knapp, Stefan  
 APPLICANT: Hauser, Hans-Peter  
 TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
 FILE REFERENCE: 05495\_0001-04  
 CURRENT APPLICATION NUMBER: US/09/886,159  
 CURRENT FILING DATE: 2001-06-22  
 PRIOR APPLICATION NUMBER: US/09/109,916  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
 PRIOR FILING DATE: 1992-10-06  
 PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
 PRIOR FILING DATE: 1992-12-30  
 PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
 PRIOR FILING DATE: 1993-06-01  
 NUMBER OF SEQ ID NOS: 67  
 SOFTWARE: Patentin ver. 2.0  
 SEQ ID NO 59  
 LENGTH: 498  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus  
 US-09-886-150-59

Query Match 49.4%; Score 40; DB 9; Length 498;  
 Best Local Similarity 44.4%; Pred. No. 25;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 EEKPLTTAAAXAPVXNA 19  
 Db 119 EETSPROTSONYPIVTNA 136

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RESULT 8  
 US-09-952-432A-2  
 Sequence 2, Application US/09952432A  
 PATENT NO. US20030150588A1  
 GENERAL INFORMATION:  
 APPLICANT: Allisson, James P.  
 APPLICANT: Fasso, Marcela  
 APPLICANT: Shastri, Nilabh  
 APPLICANT: The Regents of the University of California  
 TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN  
 FILE REFERENCE: 018341-001110US  
 CURRENT APPLICATION NUMBER: US/09/952,432A  
 CURRENT FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: 60/234,472  
 PRIORITY FILING DATE: 2000-09-21  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2  
 LENGTH: 155  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: SPAS-1 cDNA  
 US-09-952-432A-2

Query Match 48.1%; Score 39; DB 10; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 9.8;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 60 SPTTTAATMPVV 71

RESULT 9

Query Match 48.1%; Score 39; DB 10; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 9.8;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 60 SPTTTAATMPVV 71

Patent No. US20020150588A1  
 GENERAL INFORMATION:  
 APPLICANT: Allison, James P.  
 APPLICANT: Fassio, Marcella  
 APPLICANT: Shastri, Nilabh  
 APPLICANT: The Regents of the University of California  
 TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN  
 FILE REFERENCE: 018941-001110US  
 CURRENT APPLICATION NUMBER: US/09/952,432A  
 CURRENT FILING DATE: 2002-04-15  
 PRIOR APPLICATION NUMBER: 60/234,472  
 PRIOR FILING DATE: 2000-09-21  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 16  
 LENGTH: 155  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: description of Artificial Sequence:Predicted AA

Query Match 48.1%; Score 39; DB 10; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 9.8;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 60 SPTTTAATMPVV 71

RESULT 10

Query Match 48.1%; Score 39; DB 10; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 9.8;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 60 SPTTTAATMPVV 71

US-09-738-626-5663  
 Sequence 5663, Application US/09738626  
 Publication No. US20020197605A1  
 GENERAL INFORMATION:  
 APPLICANT: NAKAGAWA, SATOSHI  
 APPLICANT: MIZOGUCHI, HIROSHI  
 APPLICANT: ANDO, SEIKO  
 APPLICANT: HAYASHI, MIKIRO  
 APPLICANT: OCHIAI, KEIKO  
 APPLICANT: YOKOI, HARUHiko  
 APPLICANT: TATESHI, NAOKO  
 APPLICANT: SENOH, AKIHIRO  
 APPLICANT: IKEDA, MASATO  
 APPLICANT: OZAKI, AKIO  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-125

RESULT 11

Query Match 48.1%; Score 39; DB 9; Length 233;  
 Best Local Similarity 66.7%; Pred. No. 16; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 35 TPTTSPAPPV 46

US-09-952-432A-19  
 Sequence 19, Application US/09952432A  
 Patent No. US20020150588A1  
 GENERAL INFORMATION:  
 APPLICANT: Allison, James P.  
 APPLICANT: Fassio, Marcella  
 APPLICANT: Shastri, Nilabh  
 APPLICANT: The Regents of the University of California  
 TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN  
 FILE REFERENCE: 018941-001110US  
 CURRENT FILING DATE: 2002-04-15  
 PRIOR APPLICATION NUMBER: 60/234,472  
 PRIOR FILING DATE: 2000-09-21  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 19  
 LENGTH: 395  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Tumor SPAS-1  
 US-09-952-432A-19

Query Match 48.1%; Score 39; DB 10; Length 395;  
 Best Local Similarity 66.7%; Pred. No. 29; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 300 SPTTTAATMPVV 311

RESULT 12

Query Match 48.1%; Score 39; DB 10; Length 395;  
 Best Local Similarity 66.7%; Pred. No. 29; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 TPLTTAAAXAPPV 16  
 Db 300 SPTTTAATMPVV 311

US-09-952-432A-21  
 Sequence 21, Application US/09952432A  
 Patent No. US20020150588A1  
 GENERAL INFORMATION:  
 APPLICANT: Allison, James P.  
 APPLICANT: Fassio, Marcella  
 APPLICANT: Shastri, Nilabh  
 APPLICANT: The Regents of the University of California  
 TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN  
 FILE REFERENCE: 018941-001110US  
 CURRENT APPLICATION NUMBER: US/09/952,432A  
 CURRENT FILING DATE: 2002-04-15  
 PRIOR APPLICATION NUMBER: 60/234,472

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; PRIORITY FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 21
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: No. US20020150588A1mail SPAS-1
; US-09-952-432A-21

Query Match
Best Local Similarity 48.1%; Score 39; DB 10; Length 395;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 5 TPLTTAAAXAPVW 16
Db 300 SPPPTTAATMPVW 311

RESULT 13
US-09-866-562-92
Sequence 92, Application US/098666562
; GENERAL INFORMATION:
; PATENT NO. US2002009758A1
; APPLICANT: Harlacker, Susan L.
; APPLICANT: Wang, Tongtong
; APPLICANT: Bengur, Chaitanya S.
; APPLICANT: Klie, Jennifer
; APPLICANT: Switzer, Anne
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
; FILE REFERENCE: 210121_502
; CURRENT APPLICATION NUMBER: US/09/866, 562
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO: 92
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 14
Query Match
Best Local Similarity 46.9%; Score 38; DB 10; Length 229;
Matches 11; Conservative 1; Mismatches 4; Indels 12; Gaps 1;
Qy 3 EKTPPLTAA-----XAPVWVN 18
Db 109 EKTPPLTAAATPLSLKPPRMDTARVVA 136

RESULT 15
US-09-738-626-5209
Sequence 214, Application US/097384846
; GENERAL INFORMATION:
; PATENT NO. US20020102638A1
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ12
; CURRENT APPLICATION NUMBER: US/09/754,846
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 214
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (224)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (261)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (277)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (261)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (277)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-846-214
Query Match
Best Local Similarity 46.9%; Score 38; DB 10; Length 277;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 5 TPLTTAAAXAPVWVN 19
Db 120 TPVRPAASDIVSGA 134

; PRIORITY FILING DATE: 2000-04-07
; PRIORITY APPLICATION NUMBER: JP 00/280988
; PRIORITY FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentin ver. 3.0
; SEQ ID NO: 5209
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-5209

Query Match
Best Local Similarity 46.9%; Score 38; DB 9; Length 261;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 6 PLTTAAAXAPV 15
Db 149 PLTTASASPV 158

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Fri Mar 14 09:30:10 2003

Search completed: March 14, 2003, 09:16:49  
Job time : 14 secs

us-09-359-426c-2.rapb

GenCore version 5.1.4-p5-4578  
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### Om protein - protein search, using sw model

Run on:

March 14, 2003, 09:10:24 ; Search time 18 Seconds

(without alignments)

101.475 Million cell updates/sec

Title: US-09-359-426c-2

Perfect score: 81

Sequence: 1 XEEKTPLTTAAXAPVYXNA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase : PIR\_73.\*  
1: p11;\*  
2: p1x2;\*  
3: p1x3;\*  
4: p1x4;\*

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	63	77.8	482	2 B83113	catalase PA236 [imported] - <i>Pseudomonas aeruginosa</i> (strain PA01)
2	53	65.4	484	2 A58663	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
3	48	59.3	480	2 AB0148	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
4	46	56.8	262	2 T34408	hypothetical protein H34124.2.1 - <i>Pseudomonas aeruginosa</i> (strain PA01)
5	46	56.8	262	2 E88400	ribosomal protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)
6	45	55.6	128	2 JCI273	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)
7	44	54.3	306	2 AE0963	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)
8	44	54.3	427	2 F88436	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)
9	43	53.1	483	2 S37055	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
10	42	51.9	105	2 A44639	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
11	42	51.9	321	2 T03462	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
12	42	51.9	436	2 T45107	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
13	41	50.6	132	2 T50779	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
14	41	50.6	482	2 S60757	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
15	40	49.4	171	2 T31478	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
16	40	49.4	252	2 H73469	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
17	40	49.4	258	2 AD1328	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
18	40	49.4	394	2 E87611	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
19	40	49.4	788	2 S05661	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
20	40	49.4	1360	2 T31674	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
21	39	48.8	405	2 JO2147	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
22	39	48.1	866	2 S10772	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
23	39	48.1	507	2 B87400	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
24	39	48.1	527	2 S16088	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
25	39	48.1	1353	2 T26301	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
26	38.5	47.5	1658	2 D75489	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
27	38	46.9	143	2 S68226	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
28	38	46.9	307	2 T40089	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)
29	38	46.9	307	2 A35125	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)

### ALIGNMENTS

Query	Match	Length	DB	ID	Description
1	63	77.8	2 B83113	catalase PA236 [imported] - <i>Pseudomonas aeruginosa</i> (strain PA01)	
2	53	65.4	2 A58663	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
3	48	59.3	2 AB0148	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
4	46	56.8	2 T34408	hypothetical protein H34124.2.1 - <i>Pseudomonas aeruginosa</i> (strain PA01)	
5	46	56.8	2 E88400	ribosomal protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)	
6	45	55.6	2 JCI273	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)	
7	44	54.3	2 AE0963	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)	
8	44	54.3	2 F88436	hypothetical protein F88436 - <i>Pseudomonas aeruginosa</i> (strain PA01)	
9	43	53.1	2 S37055	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
10	42	51.9	2 A44639	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
11	42	51.9	2 T03462	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
12	42	51.9	2 T45107	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
13	41	50.6	2 T50779	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
14	41	50.6	2 S60757	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
15	40	49.4	2 T31478	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
16	40	49.4	2 H73469	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
17	40	49.4	2 AD1328	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
18	40	49.4	2 E87611	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
19	40	49.4	2 S05661	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
20	40	49.4	2 T31674	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
21	39	48.8	2 JO2147	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
22	39	48.1	2 S10772	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
23	39	48.1	2 B87400	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
24	39	48.1	2 S16088	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
25	39	48.1	2 T26301	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
26	38.5	47.5	2 D75489	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
27	38	46.9	2 S68226	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
28	38	46.9	2 T40089	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	
29	38	46.9	2 A35125	catalase (EC 1.11.1.11) - <i>Pseudomonas aeruginosa</i> (strain PA01)	

hypothetical prote

peptidase, M2/M25

hypothetical prote

peptidase (M3 fam)

probable translati

protein F5804.11 |

hypothetical prote

R;Gouet, P.; Jouve, H.M.; Hajdu, J.  
submitted to the Brookhaven Protein Data Bank, June 1996

A;Reference number: A67900; PDB:2CAF  
A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A;Note: compound I  
R;Gouet, P.; Jouve, H.M.; Hajdu, J.  
submitted to the Brookhaven Protein Data Bank, July 1996

A;Reference number: A67902; PDB:2CAH  
A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A;Note: compound II, dithiotreitol reduced compound I  
R;Gouet, P.; Jouve, H.M.; Diddeberg, O.  
J. Mol. Biol. 249, 933-954, 1995

A;Title: Crystal structure of *Proteus mirabilis* PR catalase with and without bound NADPH  
A;Reference number: A58664; PMID:9311317; PMID:7791219  
A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A;Note: native Fe(II) with NADPH  
Complex: homotetrramer

A;Function: catalyzes the conversion of two molecules of hydrogen peroxide to two  
A;Description: catalyzes the conversion of two of molecules of hydrogen peroxide to two  
A;Note: this enzyme has a tightly bound NADPH cofactor  
C;Superfamily: catalase  
C;Keywords: chromoprotein; heme; homotetrramer; iron; metalloprotein; NADP; oxidoreductases  
F;53/Modified site: methionine sulfoxide (Met) #status predicted  
F;54/93, 1/2/Active site: His, Ser, Asn #status predicted  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 EKTPLTAAXPVXN 18  
Db 2 ERKKLITTAAGAPVVDN 17

RESULT 3

AB0148 catalase (EC 1.11.1.6) [imported] - *Yersinia pestis* (strain cO92)  
C;Species: *Yersinia pestis*  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AB0148  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Gill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Titure, 413, 523-527, 2001  
Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-480 <KUR>  
A;Cross references: GB:AL590842; PIDN:CAC90045.1; PID:915979266; GSDB:GN00175

C;Genetics:  
C;Gene: katA  
C;Superfamily: catalase<sup>1</sup>  
C;Keywords: oxidoreductase

Query Match 59.3%; Score 48; DB 2; Length 480;  
Best Local Similarity 68.8%; Pred. No. 1.6; 4; Indels 0; Gaps 0;  
Matches 11; Conservative 1; Mismatches 3;

Qy 3 EKTPLTAAXPVXN 18  
Db 2 ERKKLITTAAGAPVVDN 19

RESULT 4

T33408 hypothetical protein H3124.2 - *caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999  
C;Accession: T33408  
R;Latreille, P.; Wansley, P.; O'Brien, D.  
submitted to the EMBL Data Library, July 1998

A;Description: The sequence of *C. elegans* cosmid H34124.  
A;Reference number: 221340  
A;Accession: T33408  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-262 <AT>  
A;Cross-references: EMBL:AF078784; PIDN: AAC26925.1; GSDB: GN00021; CESP:H34124.2  
A;Experimental source: strain Bristol NZ; clone H34124  
A;Genetics:  
A;Gene: CESP:H34124.2  
A;Map position: 3  
A;Note: intron positions not resolved (incomplete sequence)

Query Match 56.8%; Score 46; DB 2; Length 262;  
Best Local Similarity 56.8%; Pred. No. 1.9; 4; Indels 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Db 190 KTPLTAAXPVXNA 19

RESULT 5

F88400 protein H34124.2 [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10 May 2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: F88400  
R;Anonymous: The *C. elegans* Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating bio  
A;Reference number: A75001; MUID: 9969613; PMID: 9831916  
A;Note: see websites genome.wustl.edu/gsc/c\_elegans/ and www.sanger.ac.uk/Projects/C\_e  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
A;Accession: E88400  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-262 <STO>  
A;Cross-references: GB:chr\_III; PIDN: AAC26925.1; PID:9329614; GSDB: GN00021; CESP:H3  
C;Genetics:  
A;Gene: H34124.2  
A;Map position: 3

Query Match 56.8%; Score 45; DB 2; Length 262;  
Best Local Similarity 56.2%; Pred. No. 1.9; 4; Indels 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Db 190 KTPLTAAXPVXNA 19

RESULT 6

JC1273 ribosomal protein L7/L12 - *Streptomyces antibioticus*  
C;Species: *Streptomyces antibioticus*  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C;Accession: JC1273  
R;Parra, F.; Blanco, G.; Alonso, J.M.M.; Balbin, M.; Mendez, C.; Salas, J.A.  
Gene 118, 127-129, 1992  
A;Title: Cloning and sequencing of a gene encoding the L7/L12 ribosomal protein equivalent  
A;Reference number: JC1273; MUID: 92380478; PMID: 1511874  
A;Accession: JC1273  
A;Molecule type: DNA  
A;Residues: 1-128 <PAR>  
A;Cross-references: GB:M89911; MUID: 9153436; PIDN: AAA26811.1; PID: 9153438  
C;Superfamily: *Escherichia coli* ribosomal protein L12  
C;Keywords: protein biosynthesis; ribosome

Query Match 55.6%; Score 45; DB 2; Length 128;  
 Best Local Similarity 66.7%; Pred. No. 1.3; Mismatches 4; Indels 0; Gaps 0;  
 Matches 10; Conservative 1; MisMatches 4; Map position: /

QY 2 EEKTPPLTAXXAPVV 16  
 Db 28 EEKFDVTAAAAPVV 42

**RESULT 7**  
 AE0963 probable carbohydrate kinase STY989 [imported] - *Salmonella enterica* subsp. *enterica* se  
 C;Species: *Salmonella enterica* subsp. *enterica* se  
 C;Note: this species has also been called *Salmonella typhi*  
 C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
 C;Accession: AE0963  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th., T.; Connection, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Barrar, S.; Moule, S.; O'Gaora, P.  
*Nature* 413, 848-852, 2001  
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar  
 A;Reference number: AB0502; PMID:11677608  
 A;Accession: AE0963  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-306 <PAR>  
 A;Cross-references: GB:AL513382; PIDN:CAD03201.1; PID:916504832; GSPDB:GN00176  
 C;Gene: STY989  
 C;Superfamily: ribokinase

Query Match 54.3%; Score 44; DB 2; Length 306;  
 Best Local Similarity 47.1%; Pred. No. 4.9; Mismatches 3; Indels 0; Gaps 0;  
 Matches 8; Conservative 3; MisMatches 6; Map position: /

QY 3 EKTPPLTAAAXAPVVNA 19  
 Db 84 EKVPCFSSGVATIFVNA 100

**RESULT 8**  
 F85436 hypothetical protein Atmg36970 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C;Accession: F85436  
 R;anonymous: The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999  
 A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A85001; MUID:20083488; PMID:10617198  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-127 <STO>  
 A;Cross-references: GB:NC\_001268; NID:97270646; PIDN:CAB80363.1; GSPDB:GN00140  
 C;Genetics: ATmg36970  
 A;Map position: 4

Query Match 54.3%; Score 44; DB 2; Length 427;  
 Best Local Similarity 60.0%; Pred. No. 7.1; Mismatches 9; Conservative 2; Indels 0; Gaps 0;  
 Matches 9; Map position: /

QY 2 EEKTPPLTAXXAPVV 16  
 Db 208 EEKFDVTAAAAPVV 222

**RESULT 9**  
 S37055 catalase (EC 1.11.1.6) alpha-2 chain - *Streptomyces violaceus*

Query Match 51.9%; Score 42; DB 2; Length 321;  
 Best Local Similarity 50.0%; Pred. No. 12; Map position: 3

C;Species: *Streptomyces violaceus*  
 C;Date: 10-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 04-Mar-2000  
 C;Accession: S37055  
 R;Pacey, S.; van Pee, K.H.; Vining, L.C.  
 submitted to the EMBL Data Library, August 1993  
 A;Reference number: S37055  
 A;Accession: S37055  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-483 <FAC>  
 A;Cross-references: EMBL:X74791; NID:9397888; PIDN:CAA52796.1; PID:9581780  
 A;Note: the source is designated as *Streptomyces venezuelae*  
 C;Genetics:  
 A;Start codon: GTG  
 C;Superfamily: catalase  
 C;Keywords: chromoprotease; heme; iron; metalloprotein; oxidoreductase  
 F:54.93.127/Active site: His, Ser, Asn #status predicted  
 F:37/Binding site: heme Iron (Tyr) (axial ligand) #status predicted  
 Query Match 53.1%; Score 43; DB 2; Length 483;  
 Best Local Similarity 69.2%; Pred. No. 12; Mismatches 9; Conservative 0; Map position: /  
 Matches 9; Map position: /; Indels 0; Gaps 0; MisMatches 4; Map position: /  
 QY 6 PLTTAXXAPVVNN 18  
 Db 5 PLTTEAGAPVADN 17

**RESULT 10**  
 A44639 catalase (EC 1.11.1.6) - *Streptomyces coelicolor* (fragments)  
 C;Species: *Streptomyces coelicolor*  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Oct-1997  
 C;Accession: A44639  
 R;Walker, G.  
 submitted to the Protein Sequence Database, September 1994  
 A;Reference number: A44639  
 A;Accession: A44639  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-105 <VAL>  
 C;Superfamily: catalase  
 C;Keywords: catalase

Query Match 51.9%; Score 42; DB 2; Length 105;  
 Best Local Similarity 69.2%; Pred. No. 3.4; Mismatches 9; Conservative 0; Map position: /  
 Matches 9; Map position: /; Indels 0; Gaps 0; MisMatches 4; Map position: /  
 QY 6 PLTTAXXAPVVNN 18  
 Db 7 PLTTVAGAPVDPN 19

**RESULT 11**  
 T08462 hypothetical protein F2206.250 - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 22-Oct-1999  
 C;Accession: T08462  
 R;Quétier, F.; Purmelle, B.; Boutry, M.; Goffeau, A.; Salanoubat, M.; Mewes, H.W.; Ma submitted to the Protein Sequence Database, May 1999  
 A;Reference number: Z16420  
 A;Accession: T08462  
 A;Molecule type: DNA  
 A;Residues: 1-321 <Q&E>  
 A;Cross-references: EMBL:AL050300; GSPDB:GN00061; MTSP:F2206..250  
 C;Genetics:  
 A;Experimental source: cultivar Columbia; BAC clone F2206..250  
 A;Gene: ATSP\_F2206..250  
 A;Map position: 3

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 EEKTPPLTAAXAPVXNA 19  
 |||||:  
 Db 291 EEKTPVEKTKGVEVVKKA 308

RESULT 12

T46107 hypothetical protein T25B15\_140 - *Arabidopsis thaliana*  
 C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: T46107  
 R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.  
 submitted to the Protein Sequence Database, January 2000  
 A;Reference number: Z23021  
 A;Accession: T46107  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:AL132972  
 C;Genetics: Experimental source: cultivar Columbia; BAC clone T25B15  
 C;Map position: 3  
 A;Introns: 41B71  
 A;Note: T25B15\_140

Query Match 51.9%; Score 42; DB 2; Length 436;  
 Best Local Similarity 50.0%; Pred. No. 16; Mismatches 1; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 EEKTPPLTAAXAPVXNA 19  
 |||||:  
 Db 395 EEKTPVEKKIGVPPVKKKA 412

RESULT 13

T50779 copper chaperone homolog CCH [imported] - rice  
 C;Species: *Oryza sativa* (rice)  
 C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
 C;Accession: T50779  
 R;Himelblau, E.; Mira, H.; Lin, S.J.; Culotta, V.C.; Penarrubia, L.; Amasino, R.M.  
 Plant Physiol. 117, 1227-1234, 1998  
 A;Title: Identification of a functional homolog of the yeast copper homeostasis gene ATX  
 A;Reference number: Z24450; MUID:9701579; PMID:9701579  
 A;Accession: T50779  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-132 <HIL>  
 A;Cross-references: EMBL:AF198626; PIDN:AAFI5285.1

Query Match 49.4%; Score 40; DB 2; Length 171;  
 Best Local Similarity 53.3%; Pred. No. 13; Mismatches 6; Indels 0; Gaps 0;  
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 TPLTPPLTAAXAPVXNA 19  
 |||||:  
 Db 73 TPTTTAAAPIAAVA 87

Search completed: March 14, 2003, 09:12:52  
 Job time: 21 secs

RESULT 14

S60757 catalase (EC 1.11.1.6) - *Bordetella pertussis*  
 C;Species: *Bordetella pertussis*  
 C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000  
 C;Accession: S60757  
 R;DeShazer, D.; Wood, G.E.; Friedman, R.L.  
 Mol. Microbiol. 14, 123-130, 1994  
 A;Title: Molecular characterization of catalase from *Bordetella pertussis*: identification  
 A;Reference number: S60757; MUID:95131725; PMID:7830550  
 A;Accession: S60757  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
 A;Residues: 1-182 <HFS>  
 A;Cross-references: EMBL:U07800; NID:9494943; PID:9494944  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994  
 C;Genetics:  
 A;Gene: catA  
 C;Superfamily: catalase  
 C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase  
 F:57,90,130/Active site: His, Ser, Asn #status Predicted  
 F:340/Binding site: heme iron (Tyr) (axial ligand) #status predicted  
 Query Match 50.6%; Score 41; DB 2; Length 482;  
 Best Local Similarity 75.0%; Pred. No. 27; Mismatches 3; Indels 0; Gaps 0;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LTAAAXAPVXN 18  
 |||||:  
 Db 9 LTAAAGAPVADN 20

RESULT 15

T31478 hypothetical protein F56F12.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C;Accession: T31478  
 R;Ainscough, R.  
 submitted to the EMBL Data Library, October 1999  
 A;Reference number: Z21039  
 A;Accession: T31478  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-171 <WIL>  
 A;Cross-references: EMBL:Z82273; PIDN:CAB54978.1; GSPDB:GN00022; CESP:F56F12.1  
 A;Experimental source: clone F56F12  
 C;Genetics:  
 A;Gene: CESP:F56F12.1  
 A;Map position: 4  
 A;Introns: 16/2; 50/1  
 A;Map position: 16/2; 50/1  
 Query Match 49.4%; Score 40; DB 2; Length 171;  
 Best Local Similarity 53.3%; Pred. No. 13; Mismatches 6; Indels 0; Gaps 0;  
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 TPLTPPLTAAXAPVXNA 19  
 |||||:  
 Db 73 TPTTTAAAPIAAVA 87

GenCore version 5.1.4-p5-4578  
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### Om protein - protein search, using sw model

Run on: March 14, 2003, 09:07:13 ; Search time 10 Seconds  
(without alignments)

78.805 Million cell updates/sec

Title: US-09-359-426c-2

Perfect score: 81

Sequence: 1 XEEKTPLTTAAXAPVVXNA 19

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	77.8	482	1 CATA_PSEAE	052762 pseudomonas P43221 proteus mir RLV_STRL
2	53	65.4	484	1 CATA_PROMI	55.1 P33569 streptomyce P40022 bordetellae
3	45	55.6	128	1 CATA_DORPE	41.0 ACM1_DROME
4	43	53.1	483	1 H2B_ABAG2	40.4 agaricus bi DMPC_PSESP
5	41	50.6	482	1 PLD_CORPS	39.1 VNUC_INBLE
6	40	49.4	722	1 PLD_CORPS	39.1 GYBR_MYXNA
7	39	48.1	143	1 PLD_CORPS	39.1 GBP_9_PSESP
8	39	48.1	486	1 PLD_CORPS	39.1 corynebacterium P33314 saccharolyticum
9	39	48.1	527	1 PLD_CORPS	39.1 VNUC_INBLE
10	39	48.1	560	1 PLD_CORPS	39.1 GYBR_MYXNA
11	39	48.1	815	1 PLD_CORPS	39.1 GBP_9_PSESP
12	38	46.9	143	1 PLD_CORPS	38.0 PLD_CORPS
13	38	46.9	307	1 PLD_CORPS	38.0 Corynebacterium P20626
14	38	46.9	479	1 PLD_CORPS	38.0 pseudomonas O57114
15	38	46.9	695	1 PLD_CORPS	38.0 treponema p083748
16	38	46.9	747	1 PLD_CORPS	38.0 YNHA_CAEEL
17	38	46.9	1679	1 PLD_CORPS	38.0 Y1Q9_YEAST
18	37	45.7	366	1 PLD_CORPS	37.0 FTZL_PYRNO
19	37	45.7	442	1 PLD_CORPS	37.0 SDC3_MOUSE
20	37	45.7	482	1 PLD_CORPS	37.0 CATA_VIBFT
21	37	45.7	498	1 PLD_CORPS	37.0 LCYB_CAPN
22	37	45.7	500	1 PLD_CORPS	37.0 LCYB_LYCSES
23	37	45.7	500	1 PLD_CORPS	37.0 LCYB_TOBAC
24	37	45.7	500	1 PLD_CORPS	37.0 PSD3_ANOST
25	37	45.7	511	1 PLD_CORPS	37.0 DH4A_YEAST
26	37	45.7	534	1 PLD_CORPS	37.0 YATE_SCHPO
27	37	45.7	662	1 PLD_CORPS	37.0 MUC1_XENIA
28	37	45.7	946	1 PLD_CORPS	37.0 FTSK_CAMEO
29	37	45.7	1034	1 PLD_CORPS	37.0 GCSP_FLAM
30	37	45.7	1064	1 PLD_CORPS	37.0 ISK5_HUMAN
31	37	45.7	1567	1 PLD_CORPS	37.0 ICEN_XANCT
32	37	45.7	3390	1 PLD_CORPS	37.0 POLG_DEN3
33	36.5	45.1	1	CAVL_CAEEL	36.5 094051

RESULT 1		ALIGNMENTS		SEQUENCE FROM N.A.	
CATA_PSEAE	ID: CATA_PSEAE	STANDARD:	PRT:	482 AA.	
AC	052762;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Catalase (EC 1.11.1.6).				
GN	KATA OR PA4236.				
OS	Pseudomonas aeruginosa				
OC	Bacteria; Proteobacteria; gamma subdivision; pseudomonadaceae; Pseudomonas.				
OX	NCBI_TAXID=287;				
RN	[1] Nucleic Acids Res. 2003, 31, 10368148.				
RP	SEQUENCE FROM N.A.				
RC	[2] J. Bacteriol. 181:3730-3742(1999).				
RP	STRAIN=ATCC 15692 / PAOL; resistance to hydrogen peroxide in Pseudomonas aeruginosa.				
RT	MEDLINE:20437337; Pubmed=10984043;				
RL	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalki D.J., Lagrou M., Gabber R.L., Gooley L., Tolentino E., Westbroek-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.; RT				
RT	Complete genome sequence of Pseudomonas aeruginosa PAOL, an opportunistic pathogen.				
RL	Nature 406:959-964 (2000).				
CC	-1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.				
CC	-1- CATALYTIC ACTIVITY: 2 H(2)O2 = O(2) + 2 H(2)O.				
CC	-1- COFACTOR: Heme group.				
CC	-1- ENZYME REGULATION: BY PEROXIDE AND BFR-BOUND IRON.				
CC	-1- SUBUNIT: HETEROOMULTIMER POSSIBLY AN ALPHA(2)BETA-HETEROOTRIMER WHERE THE ALPHA SUBUNIT IS A 56 kDa PROTEIN AND THE BETA SUBUNIT A 45 kDa PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.				
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CC	EMBL; AE0040841; AAC03118.1; -				
DR	HSSP; P42321; 2CAE.				

DR	InterPro; IPR002226; Catalase.
DR	pfam; PF00199; catalase; 1.
DR	PRINTS; PS00057; CATALASE.
DR	PRODOM; PDO0510; catalase; 1.
DR	PROSITE; PS00437; CATALASE_1; 1.
DR	PROSITE; PS00438; CATALASE_2; 1.
KW	oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
KW	Complete proteome; ACT SITE 55 BY SIMILARITY.
FT	ACT SITE 128 BY SIMILARITY.
FT	ACT SITE 128 BY SIMILARITY.
FT	BINDING 338 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ	SEQUENCE 482 AA; 55589 MW; 84E5ABA647CAB414 CRC64;
QY	2 EEKTLPLTTAXAPVYN 18
QY	2 EEKTLPLTTAGAPVVDN 18
DB	Best Local Similarity 82.4%; Pred. No. 0.026; Mismatches 3; Indels 0; Gaps 0;
RESULT 2	
CATA_PROMI	
ID	CATA_PROMI STANDARD; PRT; 484 AA.
AC	P42321; 01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	Catalase (EC 1.11.1.6).
GN	KATA.
OS	proteus mirabilis.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC	Proteus.
OX	NCBI_TaxID=584;
RN	[1] SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
RP	STRAIN=PR;
RX	MEDLINE=95305957; PubMed=7786407;
RA	Buzyn A., Bracchi V., Sterladek R., Chroboczek J., Thibault P., Gagnon J., Jouve H.-M., Hudry-Clergeon G.;
RT	"Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a methionine sulfoxide in the close proximity of the active site"; J. Protein Chem. 14:59-72(1995). [2]
RL	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP	STRAIN=PR;
RC	MEDLINE=9511317; PubMed=7791219; Gouet P., Jouve H.-M., Dideberg O.; "Crystal structure of Proteus mirabilis PR catalase with and without bound NADPH." J. Mol. Biol. 249:933-954 (1995).
RT	-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
RL	-!- COFACTOR: HEME GROUP AND NADP.
CC	-!- SUBUNIT: HOMOTETRAMER.
CC	-!- SUBCELLULAR LOCATION: Cyttoplasmic.
CC	-!- MASS SPECTROMETRY: MM=55643; MW_ER=5; METHOD=Electrospray.
CC	-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
DR	PIam; PR00199; catalase; 1.
DR	PRINTS; PR00067; CATALASE.
DR	PRODOM; PDO00510; Catalase; 1.
DR	PROSITE; PS00437; CATALASE_1; 1.
DR	PDB; 2CAF; 07-DEC-96.
DR	PDB; 2CAG; 07-DEC-96.
DR	PDB; 2CAH; 11-JAN-97.
DR	InterPro; IPR002226; Catalase.
DR	Pfam; PR00199; catalase; 1.
DR	PRINTS; PR00067; CATALASE.
DR	PRODOM; PDO00510; Catalase; 1.
DR	PROSITE; PS00437; CATALASE_1; 1.
KW	oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP; 3D-structure.
FT	MOD_RES 53 53 METHIONINE SULFONE.
FT	ACT_SITE 54 54
FT	ACT_SITE 127 127
FT	BINDING 337 337 PROXIMAL HEME LIGAND.
SQ	SEQUENCE 484 AA; 555614 MW; ADC225F3CB41F5CC50 CRC64;
QY	2 EEKTLPLTTAXAPV 16
QY	2 EEKTLPLTTAGAPVVDN 42
DB	Best Local Similarity 75.0%; Pred. No. 0.13; Mismatches 0; Indels 4; Gaps 0;
RESULT 3	
RL7_STRAT	
ID	RL7_STRAT STANDARD; PRT; 128 AA.
AC	P29342; 01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	50S ribosomal protein L7/L12.
GN	RPLL.
OS	Streptomyces antibioticus.
OC	Bacteria; Actinobacteria; Actinomycetales; Streptomyctaceae; Streptomyces.
OC	Actinomycetales; Streptomyicinae; Streptomyctaceae; Streptomyces.
OX	NCBI_TaxID=1890; [1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=92380418; PubMed=1511874; Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.;
RA	"Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equivalent of Streptomyces antibioticus.";
RT	Gene 118:127-129(1992).
CC	-!- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).
CC	-!- SIMILARITY BELONGS TO THE L12 FAMILY OF RIBOSOMAL PROTEINS.
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CC	-----
DR	EMBL; M89911; AA26911.1.
DR	PIR; JCI1273; JCI1273.
DR	HSSP; P02392; ICF.
DR	Intex-Pro; IPR00206; Ribosomal_L12.
DR	Pfam; PF00542; Ribosomal_L12; 1.
DR	PRODOM; PDO01346; Ribosomal_L12; 1.
DR	TIGRFMS; TIGR0855; L12; 1.
KW	Ribosomal_protein.
SQ	SEQUENCE 128 AA; 1327 MW; F5C3EE4F45D606E8 CRC64;
QY	2 EEKTLPLTTAXAPV 16
QY	2 EEKTLPLTTAGAPVVDN 42
DB	Best Local Similarity 66.7%; Pred. No. 0.74; Mismatches 4; Indels 0; Gaps 0;
RESULT 4	
BCA_STRLV	
ID	BCA_STRLV STANDARD; PRT; 483 AA.
AC	P33569;
DT	01-FEB-1994 (Rel. 28, Last sequence update)

DE 01-OCT-1996 (Rel. 34, Last annotation update)
 CC bromoperoxidase-catalase (EC 1.11.1.-).
 GN
 OS Streptomyces violaceus (Streptomyces venezuelae).
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 NCBI\_TAXID=1936;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AVCC 10712 / ISP5230;
 RX MEDLINE=9702081; PubMed=8868441;
 RA Facy S., Gross F., Vining L.C., Yang K., van Pee K.-H.; -
 RT "Cloning, sequencing and disruption of a bromoperoxidase-catalase gene in Streptomyces venezuelae: evidence that it is not required for chlorination in chloramphenicol biosynthesis.";
 RL Microbiology 142:655-665(1996).
 CC -!- CATALYTIC ACTIVITY:  $2 \text{ H}_2\text{O}(2) \rightarrow \text{O}(2) + 2 \text{ H}_2\text{O}$ .
 CC -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U07800; AAA18481.1; -
 DR IISPP; P42321; 2CAE.
 DR InterPro; IPR002226; Catalase.
 DR PR00199; catalase; 1.
 DR PRINTS; PR00067; CATALASE.
 DR PRODOM; PD000510; CATALASE; 1.
 DR PROSITE; PS00437; CATALASE; 1; 1.
 DR PROSITE; PS00438; CATALASE; 2; 1.
 DR PROSITE; PS00439; CATALASE; 2; 1.
 DR KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT\_SITE 57 57 BY SIMILARITY.
 FT ACT\_SITE 130 130 BY SIMILARITY.
 FT BINDING 340 340 PROXIMAL HEME LIGAND (BY SIMILARITY).
 SQ 482 AA; 54508 MN; TCB73E0975C219F CRC64;

Query Match 53.1%; Score 43; DB 1; Length 482;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 9; Conservative 0; Mismatches 3; Indels 0;
 Gaps 0;

Qy 7 LTTRAXAPVXN 18
 Db 9 LTTRAGAPVADN 20

**RESULT 5**

ID	CATA_BORPE	STANDARD	PRT	482 AA.
AC	P48062;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Catalase (EC 1.11.1.6).			
GN	KATA.			
OS	Bordetella pertussis.			
OC	Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;			
OC	Bordetellaceae.			
OC	NCBI_TAXID=520;			
[1]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Oregon-R;			
RX	MEDLINE=90046926; PubMed=2510174;			
RA	Shapiro R.T., Wakimoto B.T., Subers E.M., Nathanson N.M.;			
RT	"Characterization and functional expression in mammalian cells of genomic and cDNA clones encoding a Drosophila muscarinic acetylcholine receptor,"			
RT	RT acetylcholine receptor;"			
RT	RT Proc. Natl. Acad. Sci. U.S.A. 86:9039-9043(1989).			
[2]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90005981; PubMed=2507354;			
RA	Onai T., Fitzgerald M.G., Arakawa S., Cocayne J.D., Urquhart D.A., Hall L.M., Fraser C.M., McCormick W.R., Venter J.C.;			
RT	"Cloning, sequence analysis and chromosome localization of a Drosophila muscarinic acetylcholine receptor,"			
RT	RT FEBS Lett. 255:219-225(1989).			
RL				

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CC	FlyBase; FBgn0000037; MACR_60C.
DR	InterPro; IPR00276; GPCR_Riodpsn.
DR	Pfam; PF0001; 7tm_1; 1.
PRINTS; PR0237; GPCR_RHODPSN.	
DR	PROSITE; PS0227; G-PROTEIN_RECER_FL_1; 1.
DR	PROSITE; PS50262; G-PROTEIN_RECER_FL_2; 1.
KW	Postsynaptic membrane; Multigene family; Glycoprotein; Transmembrane; Postsynaptic membrane; Ionic channel; G-protein coupled receptor.
DOMAIN	1 26 DOMAIN 82 100
TRANSMEM	26 49 TRANSMEM 101 120
FT	1 49 CYTOPLASMIC (POTENTIAL).
FT	2 60 CYTOPLASMIC (POTENTIAL).
TRANSMEM	61 81 TRANSMEM 121 140
FT	3 60 CYTOPLASMIC (POTENTIAL).
FT	4 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	141 162 TRANSMEM 163 184
FT	4 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	185 208 TRANSMEM 209 234
FT	5 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	235 256 TRANSMEM 257 276
FT	6 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	276 295 TRANSMEM 296 314
FT	7 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	315 334 TRANSMEM 335 354
FT	8 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	355 374 TRANSMEM 375 394
FT	9 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	395 414 TRANSMEM 415 434
FT	10 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	435 454 TRANSMEM 455 474
FT	11 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	475 494 TRANSMEM 495 514
FT	12 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	515 534 TRANSMEM 535 554
FT	13 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	555 574 TRANSMEM 575 594
FT	14 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	595 614 TRANSMEM 615 634
FT	15 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	635 654 TRANSMEM 655 674
FT	16 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	675 694 TRANSMEM 695 714
FT	17 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	715 734 TRANSMEM 735 754
FT	18 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	755 774 TRANSMEM 775 794
FT	19 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	795 814 TRANSMEM 815 834
FT	20 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	835 854 TRANSMEM 855 874
FT	21 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	875 894 TRANSMEM 895 914
FT	22 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	915 934 TRANSMEM 935 954
FT	23 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	955 974 TRANSMEM 975 994
FT	24 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	995 1014 TRANSMEM 1015 1034
FT	25 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1035 1054 TRANSMEM 1055 1074
FT	26 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1075 1094 TRANSMEM 1095 1114
FT	27 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1115 1134 TRANSMEM 1135 1154
FT	28 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1155 1174 TRANSMEM 1175 1194
FT	29 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1195 1214 TRANSMEM 1215 1234
FT	30 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1235 1254 TRANSMEM 1255 1274
FT	31 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1275 1294 TRANSMEM 1295 1314
FT	32 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1315 1334 TRANSMEM 1335 1354
FT	33 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1355 1374 TRANSMEM 1375 1394
FT	34 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1395 1414 TRANSMEM 1415 1434
FT	35 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1435 1454 TRANSMEM 1455 1474
FT	36 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1475 1494 TRANSMEM 1495 1514
FT	37 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1515 1534 TRANSMEM 1535 1554
FT	38 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1555 1574 TRANSMEM 1575 1594
FT	39 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1595 1614 TRANSMEM 1615 1634
FT	40 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1635 1654 TRANSMEM 1655 1674
FT	41 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1675 1694 TRANSMEM 1695 1714
FT	42 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1715 1734 TRANSMEM 1735 1754
FT	43 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1755 1774 TRANSMEM 1775 1794
FT	44 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1795 1814 TRANSMEM 1815 1834
FT	45 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1835 1854 TRANSMEM 1855 1874
FT	46 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1875 1894 TRANSMEM 1895 1914
FT	47 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1915 1934 TRANSMEM 1935 1954
FT	48 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1955 1974 TRANSMEM 1975 1994
FT	49 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	1995 2014 TRANSMEM 2015 2034
FT	50 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2035 2054 TRANSMEM 2055 2074
FT	51 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2075 2094 TRANSMEM 2095 2114
FT	52 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2115 2134 TRANSMEM 2135 2154
FT	53 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2155 2174 TRANSMEM 2175 2194
FT	54 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2195 2214 TRANSMEM 2215 2234
FT	55 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2235 2254 TRANSMEM 2255 2274
FT	56 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2275 2294 TRANSMEM 2295 2314
FT	57 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2315 2334 TRANSMEM 2335 2354
FT	58 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2355 2374 TRANSMEM 2375 2394
FT	59 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2395 2414 TRANSMEM 2415 2434
FT	60 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2435 2454 TRANSMEM 2455 2474
FT	61 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2475 2494 TRANSMEM 2495 2514
FT	62 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2515 2534 TRANSMEM 2535 2554
FT	63 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2555 2574 TRANSMEM 2575 2594
FT	64 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2595 2614 TRANSMEM 2615 2634
FT	65 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2635 2654 TRANSMEM 2655 2674
FT	66 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2675 2694 TRANSMEM 2695 2714
FT	67 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2715 2734 TRANSMEM 2735 2754
FT	68 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2755 2774 TRANSMEM 2775 2794
FT	69 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2795 2814 TRANSMEM 2815 2834
FT	70 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2835 2854 TRANSMEM 2855 2874
FT	71 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2875 2894 TRANSMEM 2895 2914
FT	72 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2915 2934 TRANSMEM 2935 2954
FT	73 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2955 2974 TRANSMEM 2975 2994
FT	74 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	2995 3014 TRANSMEM 3015 3034
FT	75 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3035 3054 TRANSMEM 3055 3074
FT	76 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3075 3094 TRANSMEM 3095 3114
FT	77 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3115 3134 TRANSMEM 3135 3154
FT	78 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3155 3174 TRANSMEM 3175 3194
FT	79 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3195 3214 TRANSMEM 3215 3234
FT	80 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3235 3254 TRANSMEM 3255 3274
FT	81 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3275 3294 TRANSMEM 3295 3314
FT	82 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3315 3334 TRANSMEM 3335 3354
FT	83 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3355 3374 TRANSMEM 3375 3394
FT	84 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3395 3414 TRANSMEM 3415 3434
FT	85 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3435 3454 TRANSMEM 3455 3474
FT	86 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3475 3494 TRANSMEM 3495 3514
FT	87 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3515 3534 TRANSMEM 3535 3554
FT	88 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3555 3574 TRANSMEM 3575 3594
FT	89 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3595 3614 TRANSMEM 3615 3634
FT	90 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3635 3654 TRANSMEM 3655 3674
FT	91 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3675 3694 TRANSMEM 3695 3714
FT	92 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3715 3734 TRANSMEM 3735 3754
FT	93 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3755 3774 TRANSMEM 3775 3794
FT	94 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3795 3814 TRANSMEM 3815 3834
FT	95 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3835 3854 TRANSMEM 3855 3874
FT	96 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3875 3894 TRANSMEM 3895 3914
FT	97 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3915 3934 TRANSMEM 3935 3954
FT	98 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3955 3974 TRANSMEM 3975 3994
FT	99 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	3995 4014 TRANSMEM 4015 4034
FT	100 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4035 4054 TRANSMEM 4055 4074
FT	101 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4075 4094 TRANSMEM 4095 4114
FT	102 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4115 4134 TRANSMEM 4135 4154
FT	103 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4155 4174 TRANSMEM 4175 4194
FT	104 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4195 4214 TRANSMEM 4215 4234
FT	105 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4235 4254 TRANSMEM 4255 4274
FT	106 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4275 4294 TRANSMEM 4295 4314
FT	107 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4315 4334 TRANSMEM 4335 4354
FT	108 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4355 4374 TRANSMEM 4375 4394
FT	109 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4395 4414 TRANSMEM 4415 4434
FT	110 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4435 4454 TRANSMEM 4455 4474
FT	111 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4475 4494 TRANSMEM 4495 4514
FT	112 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4515 4534 TRANSMEM 4535 4554
FT	113 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4555 4574 TRANSMEM 4575 4594
FT	114 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4595 4614 TRANSMEM 4615 4634
FT	115 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4635 4654 TRANSMEM 4655 4674
FT	116 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4675 4694 TRANSMEM 4695 4714
FT	117 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4715 4734 TRANSMEM 4735 4754
FT	118 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4755 4774 TRANSMEM 4775 4794
FT	119 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4795 4814 TRANSMEM 4815 4834
FT	120 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4835 4854 TRANSMEM 4855 4874
FT	121 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4875 4894 TRANSMEM 4895 4914
FT	122 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4915 4934 TRANSMEM 4935 4954
FT	123 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4955 4974 TRANSMEM 4975 4994
FT	124 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	4995 5014 TRANSMEM 5015 5034
FT	125 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5035 5054 TRANSMEM 5055 5074
FT	126 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5075 5094 TRANSMEM 5095 5114
FT	127 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5115 5134 TRANSMEM 5135 5154
FT	128 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5155 5174 TRANSMEM 5175 5194
FT	129 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5195 5214 TRANSMEM 5215 5234
FT	130 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5235 5254 TRANSMEM 5255 5274
FT	131 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5275 5294 TRANSMEM 5295 5314
FT	132 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5315 5334 TRANSMEM 5335 5354
FT	133 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5355 5374 TRANSMEM 5375 5394
FT	134 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5395 5414 TRANSMEM 5415 5434
FT	135 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5435 5454 TRANSMEM 5455 5474
FT	136 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5475 5494 TRANSMEM 5495 5514
FT	137 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5515 5534 TRANSMEM 5535 5554
FT	138 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5555 5574 TRANSMEM 5575 5594
FT	139 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5595 5614 TRANSMEM 5615 5634
FT	140 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5635 5654 TRANSMEM 5655 5674
FT	141 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5675 5694 TRANSMEM 5695 5714
FT	142 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5715 5734 TRANSMEM 5735 5754
FT	143 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5755 5774 TRANSMEM 5775 5794
FT	144 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5795 5814 TRANSMEM 5815 5834
FT	145 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5835 5854 TRANSMEM 5855 5874
FT	146 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5875 5894 TRANSMEM 5895 5914
FT	147 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5915 5934 TRANSMEM 5935 5954
FT	148 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5955 5974 TRANSMEM 5975 5994
FT	149 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	5995 6014 TRANSMEM 6015 6034
FT	150 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6035 6054 TRANSMEM 6055 6074
FT	151 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6075 6094 TRANSMEM 6095 6114
FT	152 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6115 6134 TRANSMEM 6135 6154
FT	153 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6155 6174 TRANSMEM 6175 6194
FT	154 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6195 6214 TRANSMEM 6215 6234
FT	155 62 CYTOPLASMIC (POTENTIAL).
TRANSMEM	6235 6254 TRANSMEM 6255 62

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EMBL: X52805; CAA36992.1; -. DR PIR: S1072; S1072.  
DR HSSP: P20000; 1A58;  
DR Interpret: IPR020206; Aldehyde\_dehydr.  
DR Pfam: PF00171; aldehyd; 1.  
DR PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
DR PROSITE: PS00687; ALDENHIDE\_DEHYDR\_CLU; 1.  
KW Aromatic hydrocarbons catabolism; OXIDOREDUCTASE; NAD; Plasmid.  
FT ACT-SITE 288 254 BY SIMILARITY.  
FT ACT-SITE 288 288 BY SIMILARITY.  
SQ SEQUENCE 486 AA: F906FC6A185AA68 CRC64;  
Query Match 48.1%; Score 39; DB 1; Length 486;  
Best Local Similarity 52.9%; Pred. No. 30;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 EKTPPLTAAAXAPVWNA 19 DR  
Db 181 BETPLITALGEVMOAA 197

RESULT 9

YB64\_YEAST STANDARD; PRT; 527 AA.  
TD YB64\_YEAST ID VNUC\_INBIE  
AC P38314; ID VNUC\_INBLE  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 12-JUL-1998 (Rel. 36, Last annotation update)  
DE Hypothetical 57.2 kDa protein in MET8-HPC2 Intergenic region.  
GN YB64\_YEAST  
OS Saccharomyces cerevisiae (Baker's yeast)  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP RYB64\_YEAST  
RC STRAIN=S288C;  
RA Rieder M.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE OF 114-527 FROM N.A.  
RC STRAIN=S288C;  
RA Dubois E.; el Bakkouri M.; Glandsorff N.; Messenguy F.; Pierard A.; Scheeters B.; Verlendeels F.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.  
CC -1- SIMILARITY: TO YEAST YGL056C AND S.POMBE SP523.  
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.  
CC -----  
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RESULT 10

VNUC\_INBIE STANDARD; PRT; 560 AA.  
ID VNUC\_INBLE  
AC P04655;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-MAY-1992 (Rel. 22, Last annotation update)  
DE Nucleoprotein.  
GN NP.  
OS Influenza B virus (strain B/Lee/40).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus B.  
OX NCBI\_TaxID=11355;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MBDLNE=84174071; PubMed=6324462;  
RX Brieldis D.J.; Tobin M.;  
RT "Influenza B virus genome: complete nucleotide sequence of the influenza B/Lee/40 virus segment 5 encoding the RT nucleoprotein and comparison with the B/Singapore/222/79 nucleoprotein.";  
RT nucleoprotein.";  
RL Virology 133:448-455(1984).  
CC -----  
CC -1- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.  
CC -----  
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DR EMBL: K01395; AAA3689.1;  
DR InterPro: IPR002141; Flu\_NP.  
DR Pfam: PF00505; Flu\_NP; 1.

SQ SEQUENCE 560 AA: 61770 MW; 74C4FEAF9E75A695 CRC64;  
Query Match 48.1%; Score 39; DB 1; Length 560;  
Best Local Similarity 44.4%; Pred. No. 35; 3; Mismatches 7; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EKTPPLTAAAXAPVWNA 19 DR  
Db 19 EELTGTSGATRPTIKPA 36

RESULT 11

GYRB\_MWXXA STANDARD; PRT; 815 AA.  
ID GYRB\_MWXXA  
AC 033367;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE DNA gyrase subunit B (EC 5.99.1.3).  
GN GYRB  
OS Myxococcus xanthus.  
OC Bacteria; Proteobacteria; delta subdivision: Myxobacteria;  
OC Myxococcales; Cystobacterineae; Myxoccaceae; Myxococcus.  
OX NCBI\_TaxID=34;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ER-15;

RX MEDLINE=88304088; PubMed=9659935;  
 RA Paitan Y., Boulton N., Ron E.Z., Rosenberg E., Orr E.;  
 RT "Molecular analysis of the DNA gyrb gene from *Myxococcus xanthus*.";  
 RL Microbiology 144:1641-1647(1998);  
 CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-  
 CCC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE  
 CCC DNA RINGS INCLUDING CATENANES AND KNOTTED RINGS.  
 CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA  
 CCC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE  
 CCC ENZYME FORMS AN A2B2 TETRAMER.  
 CC -!- SIMILARITY: BELONGS TO THE TYPE I TOPOISOMERASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ000543; CA04176.1; -  
 DR HSSP: P05982; 1AJ6.  
 DR InterPro: IPR003594; ATPbind\_ATPase.  
 DR InterPro: IPR002288; DNA\_gyraseB\_C.  
 DR InterPro: IPR001241; DNA\_topoisom.  
 DR Pfam: PF000204; DNAP\_lntoprim.  
 DR Pfam: PF00986; DNA\_gyraseB; I.  
 DR Pfam: PF01751; Toprasm.  
 DR Pfam: PF0251B; Haptase\_c; 1.  
 DR Prodom: PD000615; DNA\_topoisoiI; 1.  
 DR Prodom: PD149633; DNA\_gyraseB\_C; 1.  
 DR SMART: SM00337; Haptase\_c; 1.  
 DR SMART: SM00433; Top2c; 1.  
 DR TIGRFAMS: TIGR01055; gyrb; 1.  
 DR PROSITE: PS00177; TOPOISOMERASE\_II; 1.  
 DR Topoisomerase; Isomerase; ATP-binding.  
 KW SEQUENCE 815 AA; 89636 MW; 3862685FB805B32 CRC64;

Query Match 48.1%; Score 39; DB 1; Length 815;  
 Best Local Similarity 66.7%; Pred. No. 52;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 EKTPLTAAAXAP 14  
 ||||| :|||  
 2 EKTPATGSAVAP 13

RESULT 12

ID	GBP_PSESE	STANDARD	PRT	143 AA.
AC	Q27913;			
DT	15-JUL-1999 (Rel. 38, created)			
DT	15-JUL-1999 (Rel. 38, last sequence update)			
DE	Growth-blocking peptide precursor (GBP).			
OS	Pseudaliaeta separata (Arthropoda).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptaria; Noctuoidea; Noctuidae; Hadeniinae; Pseudaliaeta.			
OC	NCBI_TaxID:7105;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96150377; PubMed=7498538;			
RA	Hayakawa Y., Ohnishi A., Yamamoto A., Izumi S., Tomono S.;			
RT	"Molecular cloning and characterization of cDNA for insect biogenic peptide, growth-blocking peptide.";			
RL	FEBS Lett. 376:185-189(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90033451; PubMed=2403529;			

RX MEDLINE=98316655; PubMed=9654083;  
 RA Hayakawa Y., Noguchi H.;  
 RT "Growth-blocking peptide expressed in the insect nervous system: cloning and functional characterization.";  
 RT Eur. J. Biochem. 253:810-816(1998);  
 RN [3]  
 RP STRUCTURE BY NMR OF 121-143.  
 RC TISSUE=Hemolymp;  
 RX MEDLINE=99107831; PubMed=9990941;  
 RA Alzawa T., Fujitani N., Hayakawa Y., Ohnishi A., Ohkubo T., Kumaki Y.,  
 RA Kawano K., Hikichi K., Nitto K.;  
 RT "Solution structure of an insect growth factor, growth-blocking peptide,";  
 RL J. Biol. Chem. 274:1887-1890(1999).  
 CC -!- FUNCTION: BIOPSYNTHETIC PEPTIDE THAT PREVENTS, IN LEPIDIOTERAN, THE  
 CC ONSET OF METAMORPHOSIS FROM LARVA TO PUPA. THIS GROWTH-BLOCKING  
 CC PEPTIDE HAS REPRESSIVE ACTIVITY AGAINST JUVENILE HORMONE ESTERASE.  
 CC -----  
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 CC -----  
 DR EMBL: AB012294; BAA32793.1; -  
 DR PDB: 1BQF; 99-DEC-98.  
 DR InterPro: IPR003465; GBP\_PSP.  
 DR Pfam: PF02425; GBP\_PSP; 1.  
 DR Hemolymph; Signal; 3D-structure.  
 FT SIGNAL 1  
 FT PROTEP 23 120  
 FT PEPTIDE 121 143  
 FT DISUFDID 127 139  
 FT GROWTH-BLOCKING PEPTIDE.  
 SQ Sequence 143 AA: 15256 MW; DEBF527956840BB CRC64;

Query Match 46.9%; Score 38; DB 1; Length 143;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 Matches 10; Conservative 1; Mismatches 7; Indels 2; Gaps 1;  
 QY 2 EKTPTP-LTTAAAXAPVYNA 19  
 ||||| :|||  
 Db 83 DEVTPATTTTAAAPVPA 102

RESULT 13

ID	PUD_CORP5	STANDARD	PRT	307 AA.
AC	P20625; Q59314;			
DT	01-FEB-1991 (Rel. 17, created)			
DT	01-FEB-1991 (Rel. 17, last sequence update)			
DE	phospholipase D precursor (EC 3.1.4.4) (PUD) (choline phosphatase).			
GS	Corynebacterium pseudotuberculosis.			
OC	Bacteria; Actinobacteria; Actinobacteria (class); Actinomycetidae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;			
OC	Corynebacterium; NCBI_TaxID:1719;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 25-47.			
RX	MEDLINE=90170833; PubMed=2407718;			
RA	Hodson A.L.M., Bird P., Nisbet T.T.;			
RT	"Cloning, nucleotide sequence, and expression in <i>Escherichia coli</i> of the phospholipase D gene from <i>Corynebacterium pseudotuberculosis</i> .";			
RL	J. Bacteriol. 172:1256-1261(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=bilovis / Isolate Whetton 1;			
RX	MEDLINE=90033451; PubMed=2403529;			

RN [1]  
 RA "Songer J.G., Libby S.J., Landolo J.J., Cuevas W.A.;  
 RT "Cloning and expression of the phospholipase D gene from  
 RL Corynebacterium pseudotuberculosis in Escherichia coli.";  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BIOVAR EQUI / ISOLATE 155;  
 RX MEDLINE=9525563; PubMed=7731503;  
 RA McNamara P.J., Cuevas W.A., Songer J.G.;  
 RT "Toxic phospholipases D of Corynebacterium pseudotuberculosis, C.  
 ulcerans and Arcanobacterium haemolyticum: cloning and sequence  
 homology"; Gene 156:113-118(1995).  
 RN [4]  
 RP MUTAGENESIS.  
 RC STRAIN=BIOVAR OVIS / ISOLATE WHETTEN 1;  
 RX MEDLINE=95020614; PubMed=934899;  
 RA McNamara P.J., Bradley G.A., Songer J.G.;  
 RT "Targeted mutagenesis of the phospholipase D gene results in  
 decreased virulence of Corynebacterium pseudotuberculosis.,"  
 RL Mol. Microbiol. 12:921-930(1994).  
 CC -I- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINATION AND  
 SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHINGOMYELINASE  
 AND HEMOLYTIC ACTIVITY.  
 CC -I- CATALYTIC ACTIVITY: A phosphatidylcholine + H<sub>2</sub>O → choline + a  
 phosphate.  
 CC -I- SIMILARITY: TO OTHER CORYNEBACTERIUM PHOSPHOLIPASES D.  
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 DR EMBL: L16587; AAA49410.1; -.  
 DR PIR: A35125; A35125.  
 KW Hydrolase; Lipid degradation; Magnesium; Virulence; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 307  
 FT ACT-SITE 44 44  
 FT VARIANT 5 6  
 FT VARIANT 8 8  
 FT VARIANT 189 189  
 FT VARIANT 205 205  
 FT VARIANT 270 270  
 FT VARIANT 277 277  
 SO SEQUENCE 307 AA; 33884 MW; D3B134E6FC99875 CREG64;

Query Match 46.9%; Score 38; DB 1; Length 307;  
 Best Local Similarity 61.5%; Pred. No. 28; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 PLTTAAAXAPVWN 18  
 1: ||| 1 1 1 1 |  
 DB 18 PVGNAAAAPVWN 30

RESULT 14  
 CATA\_PSEPU  
 ID CATA\_PSEPU STANDARD: PRT; 479 AA.  
 AC 05971;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Catalogue (EC 1.11.1.6).  
 KATA OR CATA.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonads.  
 NCBI\_TaxID=303;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nichols;  
 RX MEDLINE=9833270; PubMed=9665876;  
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,  
 RA Dodson R., Gwyn M., Hickey E.K., Clayton R., Ketchum K.A.,  
 RA Sodergren R.E., Harsham J.M., McLeod M.P., Salzberg S., Peterson J.,  
 RA Khalak H., Richardson D., Howell J.K., Chaudhury M., Utterback T.,  
 RA McDonald L., Arriaga P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of Treponema pallidum, the syphilis  
 spirochete," Science 281:375-388(1998).

CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION  
 OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE  
 CC RIBOSOME.  
 CC -!- SUBCELLULAR LOCATION: cytoplasmic  
 CC --!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-G/EF-2 SUBFAMILY.  
 CC  
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 CC  
 DR EMBL; AE001248; AAC65735.1; - .  
 DR HSSP; P13551; 2EFG.  
 DR TIGR; TP0367; - .  
 DR InterPro; IPR004540; EF-G.  
 DR InterPro; IPR000640; EFTU\_D2.  
 DR InterPro; IPR004161; EF\_GTPbind.  
 DR InterPro; IPR007795; EF\_GTPbind.  
 DR InterPro; IPR005225; Small\_GTP.  
 DR Pfam; PF00009; GTP\_EFtu; 1.  
 DR Pfam; PF00679; EFG\_C; 1.  
 DR Pfam; PP03144; GTP\_EFtu\_D2; 1.  
 DR PRINTS; PR00315; ELONGATINCT.  
 DR TIGRFAMS; TIGR00231; small\_GTP; 1.  
 DR TIGRFAMS; TIGR00484; EF-G; 1.  
 DR PROSITE; PS00301; EFACTOR\_GTP; 1.  
 KW Elongation factor; Protein biosynthesis; GTP-binding;  
 KW Multigene family; Complete proteome.  
 FT \_22\_ GTP (BY SIMILARITY).  
 FT NP\_BIND 15 85 GTP (BY SIMILARITY).  
 FT NP\_BIND 136 139 GTP (BY SIMILARITY).  
 FT NP\_BIND 695 AA. 76831 MW; 46529989BEF97E4E CRC64;  
 SQ SEQUENCE

Query	2 EERKPLITRAAXAPVY	Score	38	DB	1	Length	695
Best Local Similarity	60.0%	Pred.	No.	65			
Matches	9	Conservative	1	Mismatches	5	Indels	0
				Gaps	0		

Search completed: March 14, 2003, 09:11:48  
 Job time : 13 secs

Om protein - protein search, using sw model

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Title: US-09-359-426C-2  
Perfect score: 81  
Sequence: 1 XEBKTPPLTAAKAPVWNA 19

Run on: March 14, 2003, 09:09:54 ; Search time 29 Seconds  
(without alignments)  
Scoring table: BLOSUM62  
Gappen 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
otal number of hits satisfying chosen parameters: 671580  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL-21:  
 1: sp\_archaea:\*
 2: sp\_bacteria:\*
 3: sp\_fungi:\*
 4: sp\_human:\*
 5: sp\_invertebrate:\*
 6: sp\_mammal:\*
 7: sp\_mhc:\*
 8: sp\_orchanelle:\*
 9: sp\_phage:\*
 10: sp\_plant:\*
 11: sp\_rabbit:\*
 12: sp\_virus:\*
 13: sp\_vertebrate:\*
 14: sp\_unclassified:\*
 15: sp\_rvirus:\*
 16: sp\_bacteriop:\*
 17: sp\_archaeap:\*

Pred. No. 15 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	48	59.3	480	16 0826554	Q8ZGS4 Yersinia Pe
2	45	55.8	458	5 076672	076672 caenorhabdi
3	45	55.6	484	2 09RG14	09rg14 actinobacil
4	44	54.3	306	16 08XG95	Q8XG95 salmonella
5	44	54.3	314	2 09A119	09a119 escherichia
6	44	54.3	427	10 09RA00	09ra00 arribidopsis
7	44	54.3	427	10 023188	023188 arribidopsis
8	43	53.1	506	2 P77924	P77924 pseudomonas
9	43	53.1	1240	12 QDWH18	QDWH18 rat cytomeg
10	42	51.9	210	2 Q9RNU2	Q9rnu2 streptococc
11	42	51.9	211	2 Q9X6X8	Q9x6x8 streptococc
12	42	436	436	10 Q9FT45	Q9ft45 arribidopsis'
13	42	51.9	487	16 Q9RK9	Q9rk9 streptomyce
14	41	50.6	132	10 Q9SE04	Q9se04 oryza sativ
15	41	50.6	417	2 Q54272	Q54272 streptomyce
16	41	50.6	663	17 Q8ZXX0	Q8zxx0 pyrobaculum

RESULT	1	ALIGNMENTS	
Q8ZGS4	OBZGS4	PRELIMINARY;	PRT; 480 AA.
AC	OBZGS4;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DE	Catalase (EC 1.11.1.6).		
DE	KATA OR YPO1207.		
OS	Yersinia pestis.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersiniaceae.		
OX	NCBI_TAXID=632;		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CO-92 / BTOVAR ORIENTALIS;		
RX	MEDLINE=21470413; Published=11586360;		
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Selbaiah M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moulie S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413: 523-527 (2001).		
RA	"Genomic sequence of <i>Yersinia pestis</i> , the causative agent of plague.";		
RL	EMBL: AJ414147; CAC90045; 1; -.		
DR	InterPro: IPR02226; Catalase.		
DR	PFam: PF00199; catalase; 1.		
DR	Prodom: PD00050; Catalase; 1.		
DR	PROSITE: PS00438; CATALASE_2; 1.		
KW	Oxidoreductase; Peroxidase; Complete proteome;		
SO	SEQUENCE 480 AA; 55023 MW; 27A72FB0F096347E CRC64;		
Query Match	59.3%	Score 48;	DB 16; Length 480;
Best Local Similarity	68.8%	Pred. No. 8.6;	
Matches	11; Conservative 1; Mismatches 4; Indels 0; Gaps 0		



OY	3	EKTPLTAAAXAPVVA 19	Query Match Best Local Similarity 54.3%; Score 44; DB 16; Length 306; Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL: AY045887; AAC76561.1; -. KW Hypothetical protein. SQ SEQUENCE 427 AA; 46788 MW; C8B0192D315DAE41 CRC64;
Db	84	EKVPC <sup>T</sup> SSGVAPIFVNA 100	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222
RESULT 5				
ID	Q9A119	PRELIMINARY;	PRT; 314 AA.	
AC	Q9A119;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Hypothetical	34.4 kDa protein.		
OS	Escherichia coli,			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Escherichia; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
RC				
RP	SEQUENCE FROM N.A.			
RX	STRAT <sup>M</sup> AL62;			
RX	"afa-8 Gene cluster is carried by a pathogenicity island inserted into isolates.",			
RL	Infect. Immun. 69:937-948(2001).			
DR	EMBL: AF286671; AAC27331.1; -.			
DR	HSSP: P05054; IRK2.			
DR	InterPro: IPR002173; PfKB.			
DR	Pfam: PF00294; PfKB; 1.			
DR	PRINTS: PRO0950; RIBOKINASE.			
KW	Hypothetical protein.			
SQ	SEQUENCE 314 AA; 34415 MW;	2D5F7342C817E3BB CRC64;		
OY	3	EKTPLTAAAXAPVVA 19	Query Match Best Local Similarity 54.3%; Score 44; DB 2; Length 314; Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	Query Match Best Local Similarity 54.3%; Score 44; DB 10; Length 427; Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db	93	EKVPC <sup>T</sup> SSGVAPIFVNA 109	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222
RESULT 6				
ID	Q9A400	PRELIMINARY;	PRT; 427 AA.	
AC	Q9A400;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
GN	C7A10_390.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Arabidopsis; thaliana; Streptophytina; Embryophyta; Tracheophyta;			
OC	Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxonID=3702;			
RN				
RESULT 7				
ID	Q23188	PRELIMINARY;	PRT; 427 AA.	
AC	Q23188;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)		
DE	Hypothetical 46.8 kDa protein.			
GN	C7A10_390 OR NM4G36970.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophytina; Tracheophyta;			
OC	Spermatophytina; Magnoliophyta; eu dicotyledons; core eudicots; Rosidae;			
OX	EU_ARABIDOPSIS sequencing project;			
RN	Submitted (DEC-1998) to the EMBL/GenBank/DDJB databases.			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDJB databases.			
DR	EMBL; 299707; CAB16794.1; -.			
DR	EMBL; AL161590; CAB80363.1; -.			
KW	Hypothetical protein.			
SQ	SEQUENCE 427 AA; 46800 MW;	75ACC8E02D90AB554 CRC64;		
OY	2	EKTPLTAAAXAPVVA 16	Query Match Best Local Similarity 54.3%; Score 44; DB 10; Length 427; Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	Query Match Best Local Similarity 54.3%; Score 44; DB 10; Length 427; Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db	208	EKAEMT <sup>T</sup> AMOSPVV 222	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222	Db 208 EKAEMT <sup>T</sup> AMOSPVV 222
RESULT 8				
ID	P77924	PRELIMINARY;	PRT; 506 AA.	
AC	P77924;			
DT	01-FEB-1997	(TREMBLrel. 02, Created)		
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	Catalase isozyme.			
GN	KATA.			
OS	Pseudomonas fluorescens.			
OG	Plasmid pAM106.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas.			
OX	NCBI_TaxID=294;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Strain=B36;			
RX	Medline:21318967; Pubmed=11425481;			
RA	Peters M., Heiari A., Nurk A.;			
RT	"Plasmid-encoded catalase Kata, the main catalase of Pseudomonas fluorescens strain C336."			
RL	FEBS Microbiol. Lett. 200:235-240(2001).			

"Full Length cDNA of gene C7A10\_390 (GI:4006876).";

DR	EMBL; U72068; AAB17009; 1;	-	RP	SEQUENCE FROM N.A.
HSSP	P42321; CCAE.	-	RC	STRAIN=4-96; TISSUE=BLOOD;
InterPro	IPR002226; Catalase.	-	RA	Beall B., Gherardi G., Lovgren M., Tyrrell G., Facklam R., Forwick B.;
PFam	PF00195; catalase; 1.	-	RT	"Predictions of M serotype, anti-opacity factor type, and highly related strain sets based upon the variable emm and sof gene sequences.";
PRINTS	PR00067; CATALASE.	-	RT	submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR	prod000510; catalase; 1.	-	RL	Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR	PROTE; PS00438; CATALASE_2; 1.	-	DR	EMBL; AF179217; AAH55775.1; -.
KW	Plasmid.	-	KW	Signal.
SQ	SEQUENCE 506 AA; 57324 MW; F1EA728C5D41CBE CRC64;	-	NON_TER	<1 1 POTENTIAL.
Query Match	Best Local Similarity 53.1%; Score 43; DB 2; Length 506; Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	-	SIGNAL	>210 7 SERUM OPACITY FACTOR.
QY	5 TPLTTAAAXAPVWYN 18	-	CHAIN	210 8
Db	11 THLTTGAGPAVVDN 24	-	NON_TER	210 210 MW; 199C89EECF260B6A CRC64;
SULT 9	QWH8 QDDWWHB PRELIMINARY; PRT; 1240 AA.	-	FT	SEQUENCE 210 AA; 21220 MW; 199C89EECF260B6A CRC64;
AC	QDDWWHB; 01-MAR-2001 (TREMBLrel. 16, Created)	-	FT	Best Local Similarity 51.9%; Score 42; DB 2; Length 210; Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	-	FT	QY 2 EKTPPTTAAXAPV 15
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	-	FT	Db 103 EEKTPKTVTSSTPV 116
DE	Pr2.	-	RESULT 11	QDX6XB QDX6XB PRELIMINARY; PRT; 211 AA.
GN	Rat cytomegalovirus (strain Maastricht).	-	ID	QDX6XB QDX6XB PRELIMINARY; PRT; 211 AA.
OS	Rat cytomegalovirus (strain Maastricht).	-	AC	0996XB; 01-NOV-1999 (TREMBLrel. 12, Created)
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	-	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
OC	betaherpesvirinae; Mureomaglovirus.	-	DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
OX	NCBI_TaxID=79700;	-	DE	Serum opacity factor precursor (Fragment).
RN	[1]	-	OS	Streptococcus pyogenes.
RP	SEQUENCE FROM N.A.	-	OC	Bacterium; Firmicutes; Bacillus/clostridium group; Lactobacillales;
RC	STRAIN=MAASTRICHT; MEDLINE=2036625; PubMed=10906222;	-	OC	Streptococcaceae; Streptococcus.
RX	Vink C., Beukens E., Bruggeman C.A.; "Complete DNA sequence of the rat cytomegalovirus genome."; J. Virol. 74:7656-7665(2000).	-	OX	NCBI_TaxID=314;
RR	[2]	-	RN	[1]
RP	SEQUENCE FROM N.A.	-	RC	SEQUENCE FROM N.A.
RC	STRAIN=MAASTRICHT; MEDLINE=2047313; PubMed=11018281; Gruijthuijsen Y.K.; Beukens E., Bruggeman C.A., Vink C.; "The rat cytomegalovirus R89 is a highly conserved gene which expresses a spliced transcript."; Virus Res. 69:119-130(2000).	-	RA	Beall B., Gherardi G.;
RX	RL	-	RT	"The relation of Streptococcus pyogenes sof and emm gene sequence types to genetically distinct strain sets.";
RT	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.	-	RL	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RT	EMBL; AF154330; RAD36988.1; -	-	DR	EMBL; AF154330; RAD36988.1; -
RL	SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;	-	KW	NON_TER 1 1 POTENTIAL.
QY	2 EKTPPTTAAXAPV 15	-	FT	SIGNAL <1 8 SERUM OPACITY FACTOR.
Db	570 EERRELTTAGSAPV 583	-	FT	NON_TER 211 211
RESULT 10	QPNNU2 PRELIMINARY; PRT; 210 AA.	-	SQ	SEQUENCE 211 AA; 21367 MW; F475DPC6A084FE6 CRC64;
ID	QPNNU2; 01-MAY-2000 (TREMBLrel. 13, Created)	-	Query Match	53.1%; Score 43; DB 12; Length 210; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
AC	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	-	QY	2 EKTPPTTAAXAPV 14
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	-	Db	98 EEKTPKTVTSSAPV 110
DE	Serum opacity factor precursor (fragment).	-	RESULT 12	Q9FT45 Q9FT45 PRELIMINARY; PRT; 436 AA.
GN	SOF470.	-	ID	09FT45 09FT45 PRELIMINARY; PRT; 436 AA.
OS	Streptococcus pyogenes; Bacillus/Clostridium group; Lactobacillales;	-	AC	09FT45; 09FT45 PRELIMINARY; PRT; 436 AA.
OC	Bacteria; Firmicutes; Streptococcaceae; Streptococcus.	-	DT	01-MAR-2001 (TREMBLrel. 16, Created)
OC	NCBI_TaxID=1314;	-	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
RN	[1]	-	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
		-	DE	Hypothetical protein 48.1 kDa protein.
		-	CN	T25B15_140.
		-	OS	Arabidopsis thaliana (Mouse-ear cress).
		-	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX	NCBI_TAXID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Alcaraz J.P., Clebault G., Cotteet A., Mache R., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quettier F., Salanoubat M;
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project;
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; ALJ32972; CAC07928; 1; -.
DR	InterPro; IPR00782; B0593_fasciclin.
DR	InterPro; IPR000903; Nmt.
DR	Pfam; PF02469; Fasciclin; 1.
DR	PROSITE; PS00576; NMT_2; UNKNOWN_1.
KW	Hypothetical protein.
SO	SEQUENCE 436 AA; 48073 MW; 83FD94879F9855DF CRC64;
Query Match	Best Local Similarity 51.9%; Score 42; DB 10; Length 436;
Matches	50.0%; Pred. No. 74; 1; Mismatches 8; Indels 0; Gaps 0;
QY	2 EEKTPLTAAKAVVXNA 19
Db	395 EEKTPVKEKTVGPVVKKA 412
RESULT 13	
OPRJK9	
ID	OPRJK9
AC	OPRJK9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Catalase (EC 1.11.1.6).
GN	KATA OR SC00379 OR SCF62.05.
OS	Streptomyces coelicolor
OC	bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX	NCBI_TAXID=1902;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Murphy L., Harris D., Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL	[2]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=A3(2);
RC	Thomson N.R., Parkhill J., Barrell B.G., Reljandream M.A.; Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=A3(2);
RC	Medline=97003351; PubMed=8843436;
RA	Reddenbach M., Kieser H.M., Denpaite D., Eichner A., Cullum J., Kiuchi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RA	Mol. Microbiol. 21:77-96(1996).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=A3(2) / MI45;
RA	Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S., Rabbowitsch E., Rajandream M.A., Rutledge K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
RN	[5]
RP	SEQUENCE FROM N.A.
RA	Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S., Rabbowitsch E., Rajandream M.A., Rutledge K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
RESULT 14	
OPSE04	
ID	OPSE04
AC	OPSE04;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Copper chaperone homolog CCH.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryzeae; Oryza.
OC	NCBI_TAXID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline=95369102; PubMed=9701579;
RA	Himelblau E., Mira H., Lin S.-J., Culotta V.C., Penarrubia L., Amasino R.M.; "Identification of a functional homolog of the yeast copper homeostasis gene ATX1 from Arabidopsis.";
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL	Plant Physiol. 117:1227-1234(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Mira H., Penarrubia L.; "Copper chaperone from Oryza sativa.";
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF198626; AF015285.1; -.
DR	HSSP; 000244; IFE0
DR	InterPro; IPR001934; HeavyMe_transprt.
DR	Pfam; PF00403; HMA; 1.
DP	SEQUENCE 132 AA; 15094 MW; 7176EF95350A8231 CRC64;
SQ	Query Match Best Local Similarity 50.6%; Score 41; DB 10; Length 132; Matches 50.0%; Pred. No. 37; 1; Mismatches 8; Indels 0; Gaps 0;
QY	2 EEKTPLTAAKAVVXNA 19
Db	97 ERAPPITAAEPAIAAA 114
RESULT 15	
QY	2 EEKTPLTAAKAVVXNA 19
ID	054272
AC	054272;
DT	01-NOV-1995 (TREMBLrel. 01, created)
DT	01-NOV-1995 (TREMBLrel. 01, last sequence update)

DE Hypothetical aldehyde-dehydrogenase like 43.4 kDa protein  
 DE (EC 1.2.1.-).  
 OS Streptomyces hygroscopicus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;  
 OX Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces  
 NCBI\_TaxID=1912;  
 RN [1]  
 RP STRAIN=SF293;  
 RC SEQUENCE FROM N.A.  
 RX MEDLINE=93309717; PUBMED=7789803;  
 RA Hidaka T., Hidaka M., Kuzuyama T., Seto H.;  
 RT "Sequence of a P-methyltransferase-encoding gene isolated from a  
 Rb bialaphos-producing Streptomyces hygroscopicus.";  
 RL Gene 158:149-150(1995).  
 CC -I PATHWAY: BIALAPHOS BIOSYNTHESIS.  
 CC -I SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 DR EMBL: D37877; BAA07116.1; -.  
 DR HSSP: P56533; I44S.  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR pfam: PF00171; aldedh; 1.  
 PROSITE: PS00687; ALDEHYDE\_DEHADR\_GLU; UNKNOWN\_1.  
 HYPOTHEtical Protein; Oxidoreductase.  
 ACT\_SITE 187 187 BY SIMILARITY.  
 FT ACT\_SITE 221 221 BY SIMILARITY.  
 FT SEQUENCE 417 AA: 43406 MW: 9E8714F4FB654B47 CRC64;  
 Query Match 50.6%; Score 41; DB 2; Length 417;  
 Best local Similarity 52.9%; Pred. No. 1e-02;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 Qy ||||| | | : | |  
 Db 117 EKTFPLTAAFAELIEA 133  
 Search completed: March 14, 2003, 09:12:27  
 Job time : 33 secs